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```

      20      25      30
Ala Leu Lys Asn Ser Pro Lys Asn Asp Leu Val Tyr Phe Lys Gly His
      35      40      45
Asn Glu Val Asp Leu Asn Phe Asn Ala Met Leu Lys Thr Tyr Glu Asn
      50      55      60
Phe Lys Ser Asn Tyr Arg Phe Ser Val Gly Leu Lys Pro Leu Thr Glu
      65      70      75      80
Ser Pro Lys Thr Pro Ile Leu Pro Tyr Phe Ser Lys Gly Thr His Gly
      85      90      95
Asp Lys Lys Ile Gln Glu Asn Leu Leu Asn Asn Ala Leu Ile Leu Glu
      100      105      110
Lys Ser Asn Thr Leu Tyr Ala Gln Leu Gln Pro Leu Lys Pro Ala Leu
      115      120      125
Asp Ser Pro Asn Ile Gln Val Tyr Leu Ala Phe Tyr Pro Ser Gln Ser
      130      135      140
Gln Pro Arg Leu Leu Gly Thr Leu Asp Cys Lys Asn Ala Cys Glu Pro
      145      150      155      160
Leu Lys Phe Asp Leu Leu Glu Gly Asp Lys Val Gly Arg Tyr Lys Ile
      165      170      175
Leu Phe Lys Phe Val Phe Lys Asn Lys Glu Glu Leu Ile Leu Glu Gln
      180      185      190
Leu Ala Phe Phe Lys
      195

```

(2) INFORMATION FOR SEQ ID NO:1796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1796

```

Ala Asn Gln Phe Ala Leu Gln Phe Ser Phe Ser Asn Phe Lys His Gly
1      5      10      15
Asp Phe Thr Thr Arg Asp Phe Met Leu Tyr Ser Leu Leu Tyr Gly Tyr
      20      25      30
Phe Asn Ile Asn Leu Phe Gln Tyr Leu Thr Phe Arg Ala Gly Leu Gly
      35      40      45
Phe Phe Ile Ala Phe Phe Leu Thr Leu Phe Leu Met Pro Lys Phe Ile
      50      55      60
Leu Trp Ala Lys Ala Lys Lys Ala Asn Gln Pro Ile Ser Ser Phe Val
      65      70      75      80
Pro Ser His Gln Asn Lys Lys Asp Thr Pro Thr Met Gly Gly Ile Val
      85      90      95
Phe Val Phe Ala Thr Ile Val Ala Ser Val Leu Cys Ala Ser Leu Ser
      100      105      110
Asn Leu Tyr Val Leu Leu Gly Ile Ile Val Leu Val Gly Phe Ser Phe
      115      120      125
Val Gly Phe Arg Asp Asp Tyr Thr Lys Ile Asn Gln Gln Asn Asn Ala
      130      135      140
Gly Met Ser Ala Lys Met Lys Phe Gly Met Leu Phe Ile Leu Ser Leu
      145      150      155      160

```

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1794

```

His Met Lys Gly Leu Trp Leu Val Ile Ser Leu Val Phe Val Gly Phe
1          5          10          15
Leu Trp Ala Asn Glu Ser Tyr Val Phe Asn Asn Ser Lys Gly Arg Leu
20          25          30
Thr Glu Lys Ser Val Ala Phe Ile Glu Gly Val Ser Lys Glu Leu Tyr
35          40          45
Leu Lys Thr Gly Val Arg Phe Ala Ile Asp Met Thr Asp Phe Glu Lys
50          55          60
Asn Pro Ile Ala Leu Ala Asn Lys Lys Glu Arg Gln Ser Tyr Gln Glu
65          70          75          80
Gly Phe Leu Lys Gln Leu Lys Pro Pro Phe Val Val Phe Phe Phe Tyr
85          90          95
His Asp Ala Gln Lys Ile Glu Leu Val Ala Asn Pro Lys Asp Leu Leu
100          105          110
Asp Thr Asp Lys Ile Phe Phe Glu Lys Ile Ala Pro Leu Leu Pro Thr
115          120          125
Asn Ala Lys Glu Tyr Thr Pro Gln Arg Ile Ser Ala Met Leu Ile Asn
130          135          140
Gly Tyr Ser Val Ala Val Asp Ala Leu Ala Glu Lys Tyr His Val Asn
145          150          155          160
Ile Thr Gln Asn Phe Ser Ala Pro Lys Gly Val Thr Phe Val Lys Val
165          170          175
Val Ile Tyr Ile Leu Leu Leu Thr Leu Leu Gly Ala Phe Leu Gly Leu
180          185          190
Tyr Phe Phe Lys Lys Ser
195

```

(2) INFORMATION FOR SEQ ID NO:1795:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1795

```

Glu Gly Lys Ser Met Lys Glu Lys Asn Phe Trp Pro Leu Gly Ile Met
1          5          10          15
Ser Val Leu Ile Phe Gly Leu Gly Ile Val Val Phe Leu Val Val Phe

```

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(2) INFORMATION FOR SEQ ID NO:1793:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...265

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1793

```

Ile Phe Tyr Pro Asn Gly Tyr Asn Asn Arg Met Gly Phe Leu Lys Val
1           5           10           15
Leu Lys His Asp Ala Leu Gly Gln Val Gly Asn Ile Val Ile Gly Asn
20           25           30
Phe Leu Ile Thr Leu Thr Val Leu Ala Val Cys Phe Ser Ser Gln Ser
35           40           45
Ala Glu Glu Thr Thr Met Leu Thr Leu Ser Tyr Thr Leu Phe Phe Ile
50           55           60
Leu Gly Ala Phe Leu Leu Val Ala Ile Ser Val Gly Ala Ile Lys Asn
65           70           75           80
Leu Asn Ala Leu Phe Ser Lys Arg Gly Val Leu Ser Phe Ser Leu Pro
85           90           95
Ile Ser Leu Glu Ser Leu Leu Leu Pro Lys Ile Leu Leu Pro Met Val
100          105          110
Phe Phe Ile Phe Ser Leu Phe Trp Phe Val Ala Ser Val Arg Leu Gly
115          120          125
Tyr Tyr Leu Phe Asn Ala Gln Ser Ser Val Leu Phe Ile Leu His Thr
130          135          140
Ala Leu Lys Thr Phe Ala Leu Lys Pro Thr Lys Thr Ile Gly Val Ala
145          150          155          160
Leu Phe Leu Gly Leu Val Leu Met Lys Phe Leu Phe Val Leu Ser Val
165          170          175
Leu Asn Ala Thr Arg Ile Lys Lys Ala Arg Phe Leu Leu Gly Gly Leu
180          185          190
Leu Phe Ile Leu Val Gly Val Val Leu Glu Leu Ala Phe Asn Ser Leu
195          200          205
Leu Pro Leu Met Ser Ser Ser Leu Ser Ile Asn Glu Gly Phe Tyr Tyr
210          215          220
Phe Leu Gln Gln Gln Glu Leu Gln Glu Asn Lys Tyr Tyr Leu Leu Trp
225          230          235          240
Gly Val Asp Phe Leu Lys Ile Leu Leu Leu Tyr Gly Val Ile Arg Tyr
245          250          255
Leu Leu Thr His Lys Leu Glu Leu Asp
260          265

```

(2) INFORMATION FOR SEQ ID NO:1794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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```

Ala Ser Leu Val Pro Ala Val Gly Gly Ala Leu Ile Trp Ile Pro Ile
      245      250      255
Ala Ile Tyr Glu Leu Tyr His Gly His Val Asn Glu Ala Ile Phe Ile
      260      265      270
Val Leu Tyr Ser Ile Leu Leu Ile Gly Val Leu Ile Asp Ser Val Ile
      275      280      285
Lys Pro Ile Leu Ile Val Phe Ile Lys Lys Arg Ile Phe Lys Thr Thr
      290      295      300
Leu Lys Ile Asn Glu Ile Leu Ile Phe Phe Ser Met Ile Ala Gly Ile
305      310      315      320
Ser Gln Phe Gly Phe Trp Gly Ile Ile Val Gly Pro Thr Ile Thr Ala
      325      330      335
Phe Phe Ile Ala Leu Leu Arg Leu Tyr Glu Asn Tyr Phe Ile Gln Lys
      340      345      350
Glu Gln Lys Thr Cys Glu Cys
      355

```

(2) INFORMATION FOR SEQ ID NO:1792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1792

```

Arg Leu Asn Met Asn Tyr Lys Val Ala Ser Ala Arg Asn Ile Ala Thr
1      5      10      15
Leu Leu Phe Leu Phe Phe Ser Gln Ser Glu Ala Phe Asp Leu Gly Lys
      20      25      30
Ile Ala Lys Ile Lys Ala Gly Ala Glu Ser Phe Ser Lys Val Gly Phe
      35      40      45
Asn Asn Lys Pro Ile Asn Thr Asn Lys Gly Ile Tyr Pro Thr Glu Thr
50      55      60
Phe Met Thr Ile Met Ala Tyr Met Gln Val Asp Phe Thr Glu Leu Leu
65      70      75      80
Pro Lys Ser Ala Thr Ala Asn Gly His His Leu Asp Gly Ser Leu Gly
      85      90      95
Gly Trp Gly Gly Ala Val Ile Tyr Asp Ser Thr Lys Asp Phe Ile Asn
      100      105      110
Glu Val Thr Gly Lys Pro Tyr Gly Ala Met Thr Trp Asn Tyr Val Gly
      115      120      125
Tyr Trp Gly Gly Leu Val Gly Gln Lys Pro Trp Ala Ser Cys Gly Leu
130      135      140
Ala Thr Gly Asn Leu Thr Gln Gly Gln Tyr Asp Lys Met Thr Gln Ala
145      150      155      160
Glu Met Thr Gln Leu Ser Asn Gln Glu Ala Leu Ala Ala Ser Thr Cys
      165      170      175
Ala Lys Thr Tyr Ala Asp His Thr Arg Asn Tyr Val Ile Tyr Asn Ala
      180      185      190
Tyr Leu Arg Tyr Asn Tyr Lys Asp Ile Phe Glu Ile Arg Gly Gly Arg
195      200      205
Tyr Glu Ser Gln Arg Ile Ile

```

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```

      180      185      190
Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe Thr Leu Ala
      195      200      205
Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg Leu Phe His
      210      215      220
Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn Glu Phe Leu
      225      230      235      240
Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly Val Ala Arg
      245      250      255
Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys Asn Gly Cys
      260      265      270
Phe

```

(2) INFORMATION FOR SEQ ID NO:1791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1791

```

Phe Leu Val Gln Phe Asn Gly Asp Asn Cys Met Lys Ala Gln Tyr Phe
1      5      10      15
Phe Trp Ile Leu Phe Leu Ile Gly Phe Tyr Trp Met Leu Tyr Leu Tyr
      20      25      30
Gln Asp Phe Leu Met Asp Ala Leu Ile Ala Gly Leu Leu Cys Val Gly
      35      40      45
Leu Phe Gln Val Lys Val Phe Leu Asn Lys Arg Phe Ser Asn Val Ile
      50      55      60
Ser Ser Phe Leu Cys Val Leu Val Leu Ala Ser Val Val Ile Val Pro
      65      70      75      80
Leu Tyr Phe Ile Val Tyr Lys Gly Ser Asn Val Ile Phe Glu Ile Asn
      85      90      95
Phe Glu Lys Leu Ser Ala Leu Ile Lys Trp Leu Lys Gly Thr Ile Thr
      100      105      110
Glu Asn Leu Ser His Phe Pro Ala Ile His Asp Gly Val Ser Lys Phe
      115      120      125
Leu Glu Asn Phe Ser Ala Ala Ser Ile Thr Gly Tyr Leu Leu Lys Val
      130      135      140
Ser Ser Tyr Ile Gly Lys Tyr Ser Leu Lys Leu Val Thr Asp Ala Leu
      145      150      155      160
Phe Ile Leu Gly Leu Leu Phe Phe Phe Tyr Tyr Gly Glu Lys Phe
      165      170      175
Tyr Arg Tyr Phe Leu Gly Val Leu Pro Leu Glu Met Asn Gln Ser Lys
      180      185      190
Lys Ile Phe Glu Glu Val Ala Gly Ile Leu Arg Ile Val Leu Leu Thr
      195      200      205
Ser Leu Ile Thr Val Ile Leu Glu Gly Val Ala Phe Gly Thr Met Ile
      210      215      220
Ile Trp Phe Gly His Asp Gly Trp Ser Leu Gly Ile Leu Tyr Gly Leu
      225      230      235      240

```

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1789

```

Arg Ser Pro Pro Tyr Ser Phe Leu Phe Thr Thr Pro Glu Val Phe Val
1          5          10          15
Asn Gln His Phe Pro Trp Leu Ser Gly Ala Gly Arg Leu Val Val Lys
20          25          30
Asp Leu Ala Leu Phe Ala Gly Gly Leu Phe Val Ala Gly Phe Asp Ala
35          40          45
Lys Arg Tyr Leu Glu Gly Lys Gly Phe Cys Leu Met Asp Arg Ser Ser
50          55          60
Val Gly Ile Lys Thr Lys Cys Ser Ser Gly Cys Cys Ser
65          70          75

```

(2) INFORMATION FOR SEQ ID NO:1790:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1790

```

Trp Cys Phe Thr Asn Ile Gln Glu Ile Gly Asn Asp Phe Leu Ile Pro
1          5          10          15
Gln Ser Phe Lys Lys Lys Asp Phe Ser Asn Leu Ala Gln Gln Val Cys
20          25          30
His Arg His Glu Gly Phe Gly Ala Asp Gly Leu Val Val Leu Pro
35          40          45
Ser Lys Asp Tyr Asp Tyr Glu Trp Asp Phe Tyr Asn Ser Asp Gly Ser
50          55          60
Lys Ala Gly Met Cys Gly Asn Ala Ser Arg Cys Val Gly Leu Phe Ala
65          70          75          80
Tyr Gln His Ala Ile Ala Pro Lys Glu His Val Phe Leu Ala Gly Lys
85          90          95
Arg Glu Ile Ser Ile Arg Ile Glu Glu Pro Asn Ile Val Glu Ser Asn
100          105          110
Leu Gly Asn Tyr Gln Ile Leu Asp Thr Ile Pro Asn Leu Arg Cys Lys
115          120          125
Lys Phe Phe Thr Asn Asn Ser Val Leu Glu Asn Ile Pro Met Phe Tyr
130          135          140
Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val Lys Asn Lys
145          150          155          160
Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala Leu Arg His
165          170          175
Glu Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn Lys Glu Thr

```

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```

      275              280              285
Tyr Phe Thr Ala Gly Val Lys Glu Val Arg Ser Trp Thr Ile Lys Lys
  290              295              300
Gly Ser Ser Ala Pro Val Ala Ala Gly Val Ile His Lys Asp Phe Glu
  305              310              315
Lys Gly Phe Ile Arg Ala Glu Thr Ile Ser Tyr Asp Asp Phe Ile Ala
      325              330              335
Tyr Lys Gly Glu Ala Gly Ala Lys Glu Lys Gly Ala Leu Arg Ile Glu
      340              345              350
Gly Lys Asp Tyr Ile Val Gln Asp Gly Asp Val Leu His Phe Arg Phe
      355              360              365
Asn Val
  370

```

(2) INFORMATION FOR SEQ ID NO:1788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1788

```

Arg Asn Lys Thr Met Gln Ala Leu Lys Ser Leu Leu Glu Val Ile Thr
  1              5              10              15
Lys Leu Gln Asn Leu Gly Gly Tyr Leu Met His Ile Ala Ile Phe Ile
      20              25              30
Ile Phe Ile Trp Ile Gly Gly Leu Lys Phe Val Pro Tyr Glu Ala Glu
      35              40              45
Gly Ile Ala Pro Phe Val Ala Asn Ser Pro Phe Phe Ser Phe Met Tyr
      50              55              60
Lys Phe Glu Lys Pro Ala Tyr Lys Gln His Lys Met Ser Glu Ser Gln
      65              70              75              80
Ser Met Gln Glu Glu Met Gln Asp Asn Pro Lys Ile Val Glu Asn Lys
      85              90              95
Glu Trp His Lys Glu Asn Arg Thr Tyr Leu Val Ala Glu Gly Leu Gly
      100              105              110
Ile Thr Ile Met Ile Leu Gly Ile Leu Val Leu Leu Gly Leu Trp Met
      115              120              125
Pro Leu Met Gly Val Val Gly Gly Phe Leu Ser Leu Glu
      130              135              140

```

(2) INFORMATION FOR SEQ ID NO:1789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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```

Ile Ala Leu Phe Val Ala His Leu Gly Phe Met Asp Pro Gln Ile Gly
      85      90      95
Pro Leu Val Pro Val Leu Lys Ser Tyr Trp Leu Asn Ile His Val Ser
      100      105      110
Val Ile Thr Ala Ser Tyr Gly Phe Leu Gly Leu Cys Phe Val Leu Gly
      115      120      125
Ile Leu
      130

```

(2) INFORMATION FOR SEQ ID NO:1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1787

```

Lys Arg Leu Glu Met Gly Leu Ser Val Gly Ile Val Gly Leu Pro Asn
1      5      10      15
Val Gly Lys Ser Ser Thr Phe Asn Ala Leu Thr Lys Thr Gln Asn Ala
      20      25      30
Gln Ser Ala Asn Tyr Pro Phe Cys Thr Ile Glu Pro Asn Lys Ala Ile
      35      40      45
Val Asn Val Pro Asp Arg Arg Leu Asp Ala Leu Ala Gln Ile Val Lys
      50      55      60
Pro Glu Arg Ile Leu His Ser Val Val Glu Phe Val Asp Ile Ala Gly
      65      70      75      80
Leu Ile Lys Gly Ala Ser Lys Gly Glu Gly Leu Gly Asn Gln Phe Leu
      85      90      95
Ala Asn Ile Lys Glu Cys Glu Val Ile Leu Gln Val Val Arg Cys Phe
      100      105      110
Glu Asp Asp Asn Ile Thr His Val Asn Asp Lys Ile Asp Pro Leu Asn
      115      120      125
Asp Ile Glu Thr Ile Glu Leu Glu Leu Ile Leu Ala Asp Ile Ala Thr
      130      135      140
Leu Asp Lys Arg Ile Asp Arg Leu Gln Lys Ala Leu Lys Ser Ser Lys
      145      150      155      160
Asp Ala Lys Asn Leu Leu Glu Cys Ala Leu Ser Leu Lys Thr His Leu
      165      170      175
Glu Glu Leu Lys Pro Ala Lys Thr Phe Pro Leu Asn Thr Ser Glu Ala
      180      185      190
Phe Leu Glu Leu Asp Lys Glu Leu Arg Phe Leu Ser His Lys Lys Met
      195      200      205
Ile Tyr Val Ala Asn Val Gly Glu Glu Asp Leu Asn Ile Leu Asn Glu
      210      215      220
His Ala Lys Lys Val Glu Asn His Ala Lys Val Gln Asn Ser Glu Phe
      225      230      235      240
Val Ala Leu Cys Ala Lys Leu Glu Glu Glu Met Val Ser Met Ser Gly
      245      250      255
Asp Glu Val Lys Glu Phe Leu Gln Ser Leu Gly Val Glu Glu Ser Gly
      260      265      270
Leu Glu Lys Thr Ile Arg Leu Ser Phe Lys Glu Leu Gly Leu Ile Asn

```

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```

Phe Lys Val Trp Ile Ile Ser Val Thr Gln Arg Leu Ile Thr Gly Gln
1      5      10      15
Ala Leu Leu Ser Gly Gln Phe Thr Asn Lys Glu Phe Gln Val Gly Ala
20      25      30
Tyr Ser Asn Gln Ser Ile Lys Ala Ser Ile Gly Ser Thr Thr Ser Asp
35      40      45
Lys Ile Gly Gln Val Arg Ile Ala Thr Gly Ala Leu Ile Thr Ala Ser
50      55      60
Gly Asp Ile Ser Leu Thr Phe Lys Gln Val Asp Gly Val Asn Asp Val
65      70      75      80
Thr Leu Glu Ser Val Lys Val Ser Ser Ser Ala Gly Thr Gly Ile Gly
85      90      95
Val Leu Ala Glu Val Ile Asn Lys Asn Ser Asn Arg Thr Gly Val Lys
100     105     110
Ala Tyr Ala Ser Val Ile Thr Thr Ser Asp Val Ala Val Gln Ser Gly
115     120     125
Ser Leu Ser Asn Leu Thr Leu Asn Gly Ile His Leu Gly Asn Ile Ala
130     135     140
Asp Ile Lys Lys Asn Asp Ser Asp Gly Arg Leu Val Thr Ala Ile Asn
145     150     155     160
Ala Val Thr Ser Glu Thr Gly Val Glu Ala Tyr Thr Asp Gln Lys Gly
165     170     175
Arg Leu Asn Leu Arg Ser Ile Asp Gly Arg Gly Ile Glu Ile Lys Ile
180     185     190
Asp Ser Val Ser Asn Gly Pro Ser Ala Leu Thr Lys Arg Trp Ser Lys
195     200     205
Ser Gly Gln Asp Glu Thr Lys Gly Ser Thr Asn Tyr Gly Arg Tyr Ser
210     215     220
Arg Thr Arg Leu Asp Val Arg Ala Ser Met Ser Ile Arg Tyr Leu Asn
225     230     235     240
His Ala Cys Leu Leu Gln Ser Tyr
245

```

(2) INFORMATION FOR SEQ ID NO:1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1786

```

Ser Pro Leu Trp Leu Lys Thr Arg Phe Pro Asn Ile Trp Leu Ala Lys
1      5      10      15
Ile Leu Tyr Met Ala Ile Leu Leu Cys Ala Ile Ala His Ser Val Gly
20      25      30
Leu Ile Leu Arg Trp Tyr Val Ser Gly His Ser Pro Trp Ser Asn Ala
35      40      45
Tyr Glu Ser Met Leu Tyr Ile Ala Trp Ala Ser Val Ile Ala Gly Phe
50      55      60
Val Leu Arg Ser Lys Leu Ala Leu Ser Ala Ser Ser Phe Leu Ala Gly
65      70      75      80

```

1319

Leu Ala Ile Ala Trp
115

(2) INFORMATION FOR SEQ ID NO:1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1784

Gln	Gly	Val	Thr	Thr	Met	Ala	Phe	Gln	Val	Asn	Thr	Asn	Ile	Asn	Ala	1	5	10	15
Met	Asn	Ala	His	Val	Gln	Ser	Ala	Leu	Thr	Gln	Asn	Ala	Leu	Lys	Thr	20	25	30	
Ser	Leu	Glu	Arg	Leu	Ser	Ser	Gly	Leu	Arg	Ile	Asn	Lys	Ala	Ala	Asp	35	40	45	
Asp	Ala	Ser	Gly	Met	Thr	Val	Ala	Asp	Ser	Leu	Arg	Ser	Gln	Ala	Ser	50	55	60	
Ser	Leu	Gly	Gln	Ala	Ile	Pro	Asn	Thr	Asn	Asp	Gly	Met	Gly	Ile	Ile	65	70	75	80
Gln	Val	Ala	Asp	Lys	Ala	Met	Asp	Glu	Gln	Leu	Lys	Ile	Leu	Asp	Thr	85	90	95	
Val	Lys	Val	Lys	Ala	Thr	Gln	Ala	Ala	Gln	Asp	Gly	Gln	Thr	Thr	Glu	100	105	110	
Ser	Arg	Lys	Ala	Ile	Gln	Ser	Asp	Ile	Val	Arg	Leu	Ile	Gln	Gly	Leu	115	120	125	
Asp	Asn	Ile	Gly	Asn	Thr	Thr	Tyr	Asn	Gly	Pro	Ser	Val	Ile	Val		130	135	140	
Trp	Ser	Ile	His													145			

(2) INFORMATION FOR SEQ ID NO:1785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...248

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1785

1318

```

      370              375              380
Lys Asn Ala Ser Gly Lys Ser Thr Leu Ile Asn Leu Leu Leu Gly Phe
385              390              395              400
Tyr Thr Pro Asn Ser Gly Gln Ile Ile Ile Asn Asn Lys Tyr Pro Leu
      405              410              415
Gln Asp Leu Glu Leu Asn Ser Tyr His Gln Gln Met Ser Ala Ile Phe
      420              425              430
Gln Asp Phe Ser Leu Tyr Ala Gly Tyr Ser Ile Asp Asp Asn Leu Phe
      435              440              445
Met Gln Asn Asn Ile Thr Lys Glu Gln Leu Lys Gln Lys Arg Glu Ile
      450              455              460
Leu Lys Ser Phe Asp Glu Asn Phe Gln Asn Cys Leu Asn Asp Cys Asn
465              470              475              480
Asn Thr Leu Phe Gly Ala Gln Tyr Asn Gly Val Asp Phe Ser Leu Gly
      485              490              495
Gln Lys Gln Arg Ile Ala Thr Met Arg Ala Phe Leu Lys Pro Ser Asn
      500              505              510
Cys Ile Val Leu Asp Glu Pro Ser Ser Ala Ile Asp Pro Ile Met Glu
      515              520              525
Lys Glu Phe Leu Asp Phe Ile Phe Lys Lys Ser Gln Ser Lys Met Ala
      530              535              540
Leu Ile Ile Thr His Arg Met Asn Ser Val Lys Gln Ala Asn Glu Ile
545              550              555              560
Ile Val Leu Asp Gln Gly Lys Leu Ile Glu Gln Gly Asn Phe Glu Thr
      565              570              575
Leu Met Lys Lys Gln Gly Leu Phe Cys Glu Leu Phe Leu Lys Gln Gln
      580              585              590
Tyr

```

(2) INFORMATION FOR SEQ ID NO:1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1783

```

Thr Pro Ser Met Ile Val Thr Glu Thr Ser Thr Gly Lys Ile Leu Ala
1              5              10              15
Leu Val Gly Gly Ile Asp Tyr Lys Lys Ser Ala Phe Asn Arg Ala Thr
      20              25              30
Gln Ala Lys Arg Gln Phe Gly Ser Ala Ile Lys Pro Phe Val Tyr Gln
      35              40              45
Ile Ala Phe Asp Asn Gly Tyr Ser Thr Thr Ser Lys Ile Pro Asp Thr
      50              55              60
Ala Arg Asn Phe Glu Asn Gly Asn Tyr Ser Lys Asn Ser Val Gln Asn
65              70              75              80
His Ala Trp His Pro Ser Asn Tyr Thr Arg Lys Phe Leu Gly Leu Val
      85              90              95
Thr Leu Gln Glu Ala Leu Ser His Ser Leu Asn Leu Ala Thr Ile Asn
      100              105              110

```

1317

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1782

```

Ile Arg Thr Pro Met Asp Thr Ile Lys Ser Ile Pro Ile Arg Thr Phe
1      5      10      15
Ile Leu Leu Tyr Lys Ser Ser Pro Lys Cys Val Val Leu Ala Ser Ile
20      25      30
Thr Val Leu Phe Val Gly Ile Leu Pro Ser Leu Asn Ile Leu Val Met
35      40      45
Ile Lys Leu Ile Asp Ile Val Val Asn Leu Leu Gln Lys His Thr His
50      55      60
Phe Glu Tyr Ser Leu Leu Pro Thr Leu Leu Trp Gly Ala Leu
65      70      75      80
Leu Phe Leu Thr His Val Phe Ser Gly Ile Leu Ser Ser Leu Gln Thr
85      90      95
Ile Ile Ala Glu Gln Phe Ser Ile Asn Ile Ile Thr Gln Leu Ala Asn
100     105     110
Lys Leu Thr Gln Val Lys Asn Leu Asn Phe Phe Glu Asn Lys Asp His
115     120     125
Thr Ile Lys Leu Asn Thr Ile His Asn Gly Leu His Ile Arg Pro Leu
130     135     140
Asn Tyr Val Ser Asn Leu Phe Phe Asn Leu Gln Arg Ile Ile Gly Leu
145     150     155     160
Ile Ser Leu Phe Gly Ile Leu Phe Ser Ile Ser Ile Tyr Leu Pro Phe
165     170     175
Ile Met Ile Phe Ala Thr Val Pro Cys Ile Leu Ile Ser Asn His Ile
180     185     190
Ala Lys Lys His Ser Ala Ser Ile Asp Lys Leu Gln Asp Gln Lys Glu
195     200     205
Ser Met Gln Asn Tyr Leu Tyr Ser Gly Leu Asp Asn Gln Lys Asn Lys
210     215     220
Asp Asn Leu Leu Phe Asn Phe Met Leu Asn Phe His His Lys Phe Ile
225     230     235     240
Glu Thr Lys Glu Leu Tyr Leu Asn Asn Phe Val Lys Val Ala Gln Lys
245     250     255
Asn Leu Ile Phe Thr Ile Tyr Ala Asp Val Leu Ile Thr Thr Leu Ser
260     265     270
Ile Ala Leu Phe Phe Leu Met Val Phe Ile Ile Leu Ser Lys Leu Ile
275     280     285
Gly Val Gly Ala Ile Ala Gly Tyr Ile Gln Ala Phe Ser Ser Thr Gln
290     295     300
Gln Gln Leu Gln Asp Leu Ser Phe Tyr Gly Lys Trp Phe Phe Ala Ile
305     310     315     320
Asn Lys Tyr Phe Glu Asn Tyr Phe Cys Ile Leu Asp Tyr Lys Ile Pro
325     330     335
Lys Pro Glu Thr Gln Ile Lys Leu Glu Glu Lys Ile His Ser Ile Thr
340     345     350
Phe Glu Asn Ile Ser Phe Ser Tyr Pro Asn Ser Lys Leu Ile Phe Glu
355     360     365
Asn Phe Asn Leu Ser Leu His Ser Asn Lys Ile Tyr Ala Leu Val Gly

```

SUBSTITUTE SHEET (RULE 26)

1316

(A) LENGTH: 344 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1781

```

Glu Trp Leu Met Leu Lys Lys Ile Phe Tyr Gly Phe Ile Val Leu Phe
1      5      10      15
Leu Ile Ile Val Gly Leu Leu Ala Val Leu Val Ala Gln Val Trp Val
20      25      30
Thr Thr Asp Lys Asp Ile Ala Lys Ile Lys Asp Tyr Arg Pro Ser Val
35      40      45
Ala Ser Gln Ile Leu Asp Arg Lys Gly Arg Leu Ile Ala Asn Ile Tyr
50      55      60
Asp Lys Glu Phe Arg Phe Tyr Ala Arg Phe Glu Ile Pro Pro Arg
65      70      75      80
Phe Val Glu Ser Leu Leu Ala Val Glu Asp Thr Leu Phe Phe Glu His
85      90      95
Gly Gly Ile Asn Leu Asp Ala Val Met Arg Ala Met Ile Lys Asn Ala
100     105     110
Lys Ser Gly Arg Tyr Thr Glu Gly Gly Ser Thr Leu Thr Gln Gln Leu
115     120     125
Val Lys Asn Met Val Leu Thr Arg Glu Lys Thr Leu Thr Arg Lys Leu
130     135     140
Lys Glu Ala Ile Ile Ser Ile Arg Ile Glu Lys Val Leu Ser Lys Glu
145     150     155     160
Glu Ile Leu Glu Arg Tyr Leu Asn Gln Thr Phe Phe Gly His Gly Tyr
165     170     175
Tyr Gly Val Lys Thr Ala Ser Leu Gly Tyr Phe Lys Lys Pro Leu Asp
180     185     190
Lys Leu Thr Leu Lys Glu Ile Thr Met Leu Val Ala Leu Pro Arg Ala
195     200     205
Pro Ser Phe Tyr Asp Pro Thr Lys Asn Leu Glu Phe Ser Leu Ser Arg
210     215     220
Ala Asn Asp Ile Leu Arg Arg Leu Tyr Ser Leu Gly Trp Ile Ser Ser
225     230     235     240
Asn Glu Leu Lys Ser Ala Leu Asn Glu Val Pro Ile Val Tyr Asn Gln
245     250     255
Thr Ser Thr Gln Asn Ile Ala Pro Tyr Val Val Asp Glu Val Leu Lys
260     265     270
Gln Leu Asp Gln Leu Asp Gly Leu Lys Thr Gln Gly Tyr Thr Ile Lys
275     280     285
Leu Thr Ile Asp Leu Asp Tyr Gln Arg Leu Ala Leu Glu Ser Leu Arg
290     295     300
Phe Gly His Gln Lys Ile Leu Glu Lys Ile Ala Lys Glu Lys Pro Lys
305     310     315     320
Thr Asn Ala Ser Asn Asp Lys Asp Glu Asp Asn Leu Asn Ala Gln His
325     330     335
Asp Ser Tyr Arg Asn Glu His Arg
340

```

(2) INFORMATION FOR SEQ ID NO:1782:

1315

(B) LOCATION 1...438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1780

```

Ile Arg Asn Ala Thr Met Phe Gly Asn Lys Gln Leu Gln Leu Gln Ile
1      5      10      15
Ser Gln Lys Asp Ser Glu Ile Ala Glu Leu Lys Lys Glu Val Asn Leu
20      25      30
Tyr Gln Ser Leu Leu Asn Leu Cys Leu His Glu Gly Phe Val Gly Ile
35      40      45
Lys Asn Asn Lys Val Val Phe Lys Ser Gly Asn Leu Ala Ser Leu Asn
50      55      60
Asn Leu Glu Glu Gln Ser Val His Phe Lys Glu Asn Ala Glu Ser Val
65      70      75      80
Asn Leu Gln Gly Val Ser Tyr Ser Leu Lys Ser Gln Asn Ile Asp Gly
85      90      95
Val Gln Tyr Phe Ser Leu Ala Lys Lys Thr Gly Gly Val Gly Glu Tyr
100      105      110
His Lys Asn Asp Leu Phe Lys Thr Phe Cys Thr Ser Leu Lys Glu Gly
115      120      125
Leu Glu Asn Ala Gln Glu Ser Met Gln Tyr Phe His Gln Glu Thr Gly
130      135      140
Leu Leu Leu Asn Ala Ala Lys Asn Gly Glu Glu His Ser Asn Glu Gly
145      150      155      160
Leu Ile Thr Val Asn Lys Thr Gly Gln Asp Ile Glu Ser Leu Tyr Glu
165      170      175
Lys Met Gln Asn Ala Thr Ser Leu Ala Asp Ser Leu Asn Gln Arg Ser
180      185      190
Asn Glu Ile Thr Gln Val Ile Ser Leu Ile Asp Asp Ile Ala Glu Gln
195      200      205
Thr Asn Leu Leu Ala Leu Asn Ala Ala Ile Glu Ala Ala Arg Ala Gly
210      215      220
Glu His Gly Arg Gly Phe Ala Val Val Ala Asp Glu Val Arg Lys Leu
225      230      235      240
Ala Glu Lys Thr Gln Lys Ala Thr Lys Glu Ile Ala Val Val Val Lys
245      250      255
Ser Met Gln Gln Glu Ala Asn Asp Ile Gln Thr Asn Thr His Asp Ile
260      265      270
Asn Ser Ile Val Gly Ser Ile Lys Gly Asp Val Glu Glu Leu Lys Ser
275      280      285
Thr Val Lys Asn Asn Met Ile Val Ala Gln Ala Ala Lys Tyr Thr Ile
290      295      300
Tyr Asn Ile Asn Asn Arg Val Phe Cys Gly Leu Ala Lys Leu Asp His
305      310      315      320
Val Val Phe Lys Asn Asn Leu Tyr Gly Met Val Phe Gly Leu Asn Ser
325      330      335
Phe Asp Ile Thr Ser His Lys Ser Cys Arg Leu Gly Lys Trp Tyr Tyr
340      345      350
Glu Gly Ala Gly Lys Glu Asn Phe Ala Asn Thr Ser Gly Tyr Arg Ala
355      360      365
Leu Glu Ser His His Ala Ser Val His Ala Glu Ala Asn Asp Leu Val
370      375      380
Lys Ala Val Gln Glu Asp His Val Thr Asp Ser Lys Tyr Leu Glu His
385      390      395      400
Lys Val His Leu Met Glu Asp Ser Ala Lys His Val Lys Glu Asn Ile
405      410      415
Asp Lys Met Phe Tyr Glu Lys Gln Asp Glu Leu Asn Lys Ile Ile Glu
420      425      430
Lys Ile Gln Lys Gly Glu
435

```

(2) INFORMATION FOR SEQ ID NO:1781:

(i) SEQUENCE CHARACTERISTICS:

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1314

```

                245                250                255
Gly Asp Val Ile Gly Asp Leu Asn Arg Arg Arg Gly Gln Ile Asn Ser
                260                265                270
Met Asp Asp Arg Leu Gly Leu Lys Ile Val Asn Ala Phe Val Pro Leu
                275                280                285
Val Glu Met Phe Gly Tyr Ser Thr Asp Leu Arg Ser Ala Thr Gln Gly
                290                295                300
Arg Gly Thr Tyr Ser Met Glu Phe Asp His Tyr Gly Glu Val Pro Ser
305                310                315                320
Asn Ile Ala Lys Glu Ile Val Glu Lys Arg Lys Gly
                325                330

```

(2) INFORMATION FOR SEQ ID NO:1779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1779

```

Ser Lys Arg Ala Phe Ala Ser Ser Leu Val Ser Ser Lys Leu Phe Leu
1          5          10          15
Arg Asp Lys Glu Thr Arg Lys Arg Gly Leu Glu Thr Val Gly Gly Arg
20        25        30
Ile Ala Pro Thr Lys Asn Pro Phe Ser Phe Lys Lys Tyr Trp Ala Phe
35        40        45
Lys Arg Ala Gly Leu Phe Ser Asn Ser Arg Val Lys Asn Pro Val Gly
50        55        60
Val Leu Thr Pro Lys Val Ser Lys Ile Ile Cys Trp Cys Leu Leu Ser
65        70        75        80
Ser Phe Phe Asn Ser Cys Phe Cys Ala Ile Lys Tyr Ser Lys Trp Ala
85        90        95
Lys Val Lys Ala Val Ser Asn Arg Leu Lys Ala Val Val
100       105

```

(2) INFORMATION FOR SEQ ID NO:1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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1313

```

Val Asp Phe Tyr Arg Pro Ser Ser Ile Ala Tyr Leu Glu Leu Asp Pro
290                295                300
Arg Asp Phe Asn Ala Thr Glu Glu Trp Gln Lys Glu Asn Leu Lys Ile
305                310                315                320
Arg Ser Lys Ala Gln Ala Lys Met Leu Glu Met Arg Ser Leu Lys Pro
                325                330                335
Asp Pro Gln Ala His Leu Ser Thr Ser Gln Ser Leu Leu Leu Val Gln
                340                345                350
Lys Ile Phe Ala Asp Val Ser Lys Glu Ile Lys Val Val Ala Asn Thr
                355                360                365
Glu Lys Lys Val Glu Lys Ala Gly Tyr Gly Tyr Ser Lys Arg Met
370                375                380

```

(2) INFORMATION FOR SEQ ID NO:1778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1778

```

Asn Lys Arg Lys Asn Ile Lys Glu Val Tyr Ala Gly Glu Ile Cys Ala
1      5      10      15
Phe Val Gly Leu Lys Asp Thr Leu Thr Gly Asp Thr Leu Cys Asp Glu
20     25     30
Lys Asn Ala Val Val Leu Glu Arg Met Glu Phe Pro Glu Pro Val Ile
35     40     45
His Ile Ala Val Glu Pro Lys Thr Lys Ala Asp Gln Glu Lys Met Gly
50     55     60
Val Ala Leu Gly Lys Leu Ala Glu Glu Asp Pro Ser Phe Arg Val Met
65     70     75     80
Thr Gln Glu Glu Thr Gly Gln Thr Leu Ile Gly Gly Met Gly Glu Leu
85     90     95
His Leu Glu Ile Ile Val Asp Arg Leu Lys Arg Glu Phe Lys Val Glu
100    105    110
Ala Glu Ile Gly Gln Pro Gln Val Ala Phe Arg Glu Thr Ile Arg Ser
115    120    125
Ser Val Ser Lys Glu His Lys Tyr Ala Lys Gln Ser Gly Gly Arg Gly
130    135    140
Gln Tyr Gly His Val Phe Ile Lys Leu Glu Pro Lys Glu Pro Gly Ser
145    150    155    160
Gly Tyr Glu Phe Val Asn Glu Ile Ser Gly Gly Val Ile Pro Lys Glu
165    170    175
Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Ala Met Gln Asn Gly
180    185    190
Val Leu Ala Gly Tyr Pro Val Val Asp Phe Lys Val Thr Leu Tyr Asp
195    200    205
Gly Ser Tyr His Asp Val Asp Ser Ser Glu Met Ala Phe Lys Ile Ala
210    215    220
Gly Ser Met Ala Phe Lys Glu Ala Ser Arg Ala Ala Asn Pro Val Leu
225    230    235    240
Leu Glu Pro Met Met Lys Val Glu Val Glu Val Pro Glu Glu Tyr Met

```

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1312

```

          100          105          110
Val His Phe His Ala Pro Met Glu Phe Leu Ile Asn Asn Lys Thr Arg
          115          120          125
Pro Leu Ser Ala His Phe Val His Lys Asp Ala Lys Gly Arg Leu Leu
          130          135          140
Val Leu Ala Ile Gly Phe
          145          150

```

(2) INFORMATION FOR SEQ ID NO:1777:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1777

```

Met Pro Val Ile Arg Val Leu Val Met Leu Ala Thr Met Met Met Lys
1          5          10          15
Leu Val Lys Thr Ala Lys Glu Lys Lys Val Phe Lys Asn Val Gly Ile
          20          25          30
Ser Ile Met Gly Ile Ala Phe Trp Glu Ala Ile Lys Asp Ser Ile Lys
          35          40          45
Lys Gln Ile Lys Lys Ser Asp Trp Ile Cys Gly Asn Val Lys Thr Ala
          50          55          60
Asp Asp Tyr Leu Lys Thr His Pro Asn Ser Trp Phe Asn Ser Ala Ile
          65          70          75          80
Gly Val Thr Ala Ile Thr Ala Met Leu Met Asn Val Cys Phe Ala Asp
          85          90          95
Asp Gln Ser Lys Lys Glu Val Ala Gln Ala Gln Lys Glu Ala Glu Asn
          100          105          110
Ala Arg Asp Arg Ala Asn Lys Ser Gly Ile Glu Leu Glu Gln Glu Glu
          115          120          125
Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys
          130          135          140
Thr Glu Gln Glu Lys Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Glu
          145          150          155          160
Gln Glu Lys Gln Lys Thr Ser Asn Ile Glu Thr Asn Asn Gln Ile Lys
          165          170          175
Val Glu Gln Glu Gln Gln Lys Thr Glu Gln Glu Lys Gln Lys Thr Asn
          180          185          190
Asn Thr Gln Lys Asp Leu Val Asn Lys Ala Glu Gln Asn Cys Gln Glu
          195          200          205
Asn His Asn Gln Phe Phe Ile Lys Lys Leu Gly Ile Lys Ala Gly Ile
          210          215          220
Ala Ile Glu Ile Glu Ala Glu Cys Lys Thr Pro Lys Pro Thr Lys Thr
          225          230          235          240
Asn Gln Thr Pro Ile Gln Pro Lys His Leu Pro Asn Ser Lys Gln Pro
          245          250          255
His Ser Gln Arg Gly Ser Lys Ala Gln Glu Leu Ile Ala Tyr Leu Gln
          260          265          270
Lys Glu Leu Glu Ser Leu Pro Tyr Ser Gln Lys Ala Ile Ala Lys Gln
          275          280          285

```

SUBSTITUTE SHEET (RULE 26)

1311

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1775

```

Lys Gly Ile Gln Lys Lys Gln Asn Leu Lys Glu Val Ala Leu Asp Ala
1          5          10          15
Phe Leu Pro Lys Ser Ile Asn Tyr Tyr His Phe Asn Gly Ser Leu Thr
          20          25          30
Ala Pro Pro Cys Thr Glu Gly Val Ala Trp Phe Val Ile Glu Glu Pro
          35          40          45
Leu Glu Val Ser Ala Lys Gln Leu Ala Glu Ile Lys Lys Arg Met Lys
50          55          60
Asn Ser Pro Asn Gln Arg Pro Val Gln Pro Asp Tyr Asn Thr Val Ile
65          70          75          80
Ile Lys Ser Ser Ala Glu Thr Arg
          85

```

(2) INFORMATION FOR SEQ ID NO:1776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1776

```

Arg Ile Ile Lys Met Lys Lys Thr Phe Leu Ile Ala Leu Ala Leu Thr
1          5          10          15
Ala Ser Leu Ile Gly Ala Glu Asn Thr Lys Trp Asp Tyr Lys Asn Lys
          20          25          30
Glu Asn Gly Pro His Arg Trp Asp Lys Leu His Lys Asp Phe Glu Val
          35          40          45
Cys Lys Ser Gly Lys Ser Gln Ser Pro Ile Asn Ile Glu His Tyr Tyr
50          55          60
His Thr Gln Asp Lys Ala Asp Leu Gln Phe Lys Tyr Ala Ala Ser Lys
65          70          75          80
Pro Lys Ala Val Phe Phe Thr His His Thr Leu Lys Ala Ser Phe Glu
          85          90          95
Pro Thr Asn His Ile Asn Tyr Arg Gly His Asp Tyr Val Leu Asp Asn

```

SUBSTITUTE SHEET (RULE 26)

1310

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1774

```

Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
1      5      10      15
Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
20      25      30
Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
35      40      45
Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
50      55      60
Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65      70      75      80
Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
85      90      95
Ala Leu Ala Trp Asn Phe Trp Val Leu Leu Leu Ser Arg Met Gly Ile
100     105     110
Ala Phe Ala His Ser Ile Phe Trp Ser Ile Thr Ala Ser Leu Val Ile
115     120     125
Arg Val Ala Pro Arg Asn Lys Lys Gln Gln Ala Leu Gly Leu Leu Ala
130     135     140
Leu Gly Ser Ser Leu Ala Met Ile Leu Gly Leu Pro Leu Gly Arg Ile
145     150     155     160
Ile Gly Gln Ile Leu Asp Trp Arg Ser Thr Phe Gly Val Ile Gly Gly
165     170     175
Val Ala Thr Leu Ile Met Leu Leu Met Trp Lys Leu Leu Pro His Leu
180     185     190
Pro Ser Arg Asn Ala Gly Thr Leu Ala Ser Val Pro Ile Leu Met Lys
195     200     205
Arg Pro Leu Leu Val Gly Ile Tyr Leu Leu Val Ile Met Val Ile Ser
210     215     220
Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe Ile Ile Gln Ile
225     230     235     240
Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu Phe Val Phe Gly
245     250     255
Leu Ala Asp Val Val Gly Ser Phe Leu Phe Gly Arg Leu Tyr Ala Lys
260     265     270
Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu Val Ile Cys Pro
275     280     285
Gln Leu Leu Leu Phe Val Phe Lys Asn Leu Glu Trp Val Ile Phe Leu
290     295     300
Gln Ile Phe Leu Trp Gly Ile Gly Ile Thr Ser Leu Thr Ile Thr Leu
305     310     315     320
Gln Asn Glu Gly Ile His
325

```

(2) INFORMATION FOR SEQ ID NO:1775:

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1309

Ala Ile Thr Ile Leu Val Glu His Gly Glu Gly Gly Ser Lys Leu Gly
 500 505 510
 Gly Leu Leu Val Lys Met Ser Asn Lys Leu Tyr Glu Leu Gly Tyr Leu
 515 520 525

(2) INFORMATION FOR SEQ ID NO:1773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1773

Ile Asn Phe Val Asn Lys Gly Val Phe Met Asn Ile Phe Lys Arg Ile
 1 5 10 15
 Ile Cys Val Thr Ala Ile Val Leu Gly Phe Phe Asn Leu Leu Asp Ala
 20 25 30
 Lys His His Lys Glu Lys Lys Glu Asp His Lys Ile Thr Arg Glu Leu
 35 40 45
 Lys Val Gly Ala Asn Pro Val Pro His Ala Gln Ile Leu Gln Ser Val
 50 55 60
 Val Asp Asp Leu Lys Glu Lys Gly Ile Lys Leu Val Ile Val Ser Phe
 65 70 75 80
 Thr Asp Tyr Val Leu Pro Asn Leu Ala Leu Asn Asp Gly Ser Leu Asp
 85 90 95
 Ala Asn Tyr Phe Gln His Arg Pro Tyr Leu Asp Arg Phe Asn Leu Asp
 100 105 110
 Arg Lys Met His Leu Val Gly Leu Ala Asn Ile His Val Glu Pro Leu
 115 120 125
 Arg Phe Tyr Ser Gln Lys Ile Thr Asp Ile Lys Asn Leu Lys Lys Gly
 130 135 140
 Ser Val Ile Ala Val Pro Asn Asp Pro Ala Asn Gln Gly Arg Ala Leu
 145 150 155 160
 Ile Leu Leu His Lys Gln Gly Leu Ile Ala Leu Lys Asp Pro Ser Asn
 165 170 175
 Leu Tyr Ala Thr Glu Phe Asp Ile Val Lys Asn Pro Tyr Asn Ile Lys
 180 185 190
 Ile Lys Pro Leu Glu Ala Ala Leu Leu Pro Lys Val Leu Gly Asp Val
 195 200 205
 Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu Thr
 210 215 220
 Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu Val
 225 230 235 240
 Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu Ile
 245 250 255
 Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr Tyr
 260 265 270
 Lys Gly Ala Ile Ile Pro Ala Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:1774:

SUBSTITUTE SHEET (RULE 26)

1308

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1772

His	Glu	Phe	Leu	Ala	Ile	Asn	Glu	Leu	Met	Phe	Asp	Val	Phe	Leu	Pro
1			5					10						15	
Ser	Arg	Leu	Lys	Gln	Lys	Glu	Leu	Leu	Glu	Lys	Ile	Glu	Val	Ile	Gln
		20					25					30			
Lys	Phe	Phe	Pro	Asn	Phe	Pro	Lys	Glu	Thr	Leu	Leu	Asn	Asn	Tyr	Gln
	35						40				45				
Lys	Glu	Asn	Ser	Leu	Tyr	Asn	His	Asn	Leu	Ile	Lys	Val	Val	Gly	Phe
	50					55					60				
Ile	Pro	Tyr	Ala	Thr	Met	Gln	Ser	Leu	Tyr	Thr	Lys	Leu	Ile	Gln	Thr
65				70					75					80	
Gln	Gly	Ile	Phe	Val	Arg	Pro	Leu	Asp	Lys	Arg	Tyr	Tyr	Pro	Asn	Asn
			85						90					95	
Ala	Leu	Ala	Ser	His	Val	Leu	Gly	Tyr	Val	Gly	Val	Ala	Ser	Leu	Gln
			100					105					110		
Asp	Leu	Lys	Asp	Asp	Glu	Glu	Asn	Gln	Tyr	Ser	Gln	Ile	Val	Gly	Lys
	115						120					125			
Thr	Gly	Ile	Glu	Lys	Glu	Tyr	Asn	Lys	Phe	Leu	Gln	Gly	Lys	Val	Gly
	130					135					140				
Tyr	Lys	Ile	Ile	His	Val	Asn	Ala	Leu	Asn	Gln	Glu	Leu	Ala	Thr	Leu
145				150						155				160	
Glu	Val	Val	Pro	Pro	Arg	Ser	Asn	Asn	His	Ser	Gln	Leu	Ser	Leu	Asp
			165						170					175	
Lys	Arg	Phe	Gln	Lys	Glu	Ala	His	Lys	Leu	Phe	Val	Asn	Lys	Arg	Gly
		180						185					190		
Pro	Ile	Leu	Val	Met	Asp	Ala	Glu	Asn	Gly	Glu	Leu	Leu	Val	Ala	Gly
	195						200					205			
Ser	Tyr	Pro	Glu	Tyr	Asn	Leu	Asn	Asp	Phe	Val	Gly	Gly	Ile	Ser	Gln
	210				215						220				
Asp	Lys	Trp	Gln	Lys	Leu	Gln	Asp	Asp	Ile	Tyr	Asn	Pro	Leu	Leu	Asn
225					230					235				240	
Arg	Phe	Ala	Asn	Ala	Leu	Tyr	Pro	Pro	Gly	Ser	Val	Val	Lys	Met	Gly
			245						250					255	
Val	Gly	Leu	Ser	Phe	Leu	Glu	Asn	Leu	His	Ile	Thr	Glu	Asn	Thr	Thr
		260						265					270		
Ile	Pro	Thr	Pro	Pro	Phe	Ile	Glu	Val	Gly	Lys	Arg	Lys	Phe	Arg	Asp
	275					280						285			
Trp	Lys	Lys	Thr	Gly	His	Gly	Asn	Ser	Asn	Leu	Tyr	Lys	Ala	Ile	Arg
	290					295					300				
Glu	Ser	Val	Asp	Val	Tyr	Phe	Tyr	Lys	Phe	Gly	Leu	Glu	Ile	Ser	Ile
305					310					315				320	
Glu	Lys	Leu	Ser	Lys	Thr	Leu	Arg	Glu	Val	Gly	Phe	Gly	Glu	Lys	Thr
			325						330					335	
Gly	Val	Asp	Leu	Pro	Asn	Glu	Phe	Val	Gly	Ile	Val	Pro	Asp	Asn	Leu
		340						345					350		
Trp	Lys	Leu	Lys	Arg	Phe	Asn	Gln	Asp	Trp	Arg	Val	Gly	Asp	Thr	Leu
	355					360						365			
Ile	Thr	Ala	Ile	Gly	Gln	Gly	Ser	Phe	Leu	Ala	Thr	Pro	Leu	Gln	Val
	370					375					380				
Leu	Ala	Tyr	Thr	Gly	Leu	Ile	Ala	Thr	Gly	Lys	Leu	Ala	Thr	Pro	His
385					390					395				400	
Phe	Ala	Ile	His	Asn	Gln	Gln	Pro	Leu	Lys	Asp	Pro	Leu	Asn	Ser	Phe
			405						410					415	
Gln	Lys	Lys	Lys	Leu	Gln	Ala	Leu	Arg	Val	Gly	Met	Tyr	Glu	Val	Cys
			420					425					430		
Asn	His	Lys	Asp	Gly	Thr	Ala	Tyr	His	Ser	Thr	Arg	Gly	Ser	Lys	Val
	435					440						445			
Thr	Leu	Ala	Cys	Lys	Thr	Gly	Thr	Ala	Gln	Val	Val	Glu	Ile	Ala	Gln
	450					455					460				
Asn	Ile	Val	Asn	Arg	Met	Lys	Glu	Lys	Asp	Met	Glu	Tyr	Phe	His	Arg
465					470					475				480	
Ser	His	Ala	Trp	Ile	Thr	Ala	Phe	Leu	Pro	Tyr	Glu	Lys	Pro	Lys	Tyr
			485						490					495	

SUBSTITUTE SHEET (RULE 26)

1307

Asn Ala Leu Asp Val Phe Thr Thr Asp Ala Gln Ile Lys Glu Leu Asp
 305 310 315 320
 Leu Lys Val Leu Lys Asp Asp Lys Gly Phe Phe Pro Asn Tyr Gln Ala
 325 330 335
 Gly Ile Val

(2) INFORMATION FOR SEQ ID NO:1771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1771

Gly Ala Lys Met Lys Lys Ile Gly Leu Ser Leu Cys Leu Val Leu Ser
 1 5 10 15
 Leu Gly Phe Leu Lys Ala His Glu Val Ser Ala Glu Glu Ile Ala Asp
 20 25 30
 Ile Phe Tyr Lys Leu Asn Ala Lys Glu Pro Lys Met Lys Ile Asn His
 35 40 45
 Thr Lys Gly Phe Cys Ala Lys Gly Val Phe Leu Pro Asn Pro Gln Ala
 50 55 60
 Arg Glu Asp Leu Glu Val Pro Leu Leu Asn Glu Lys Glu Ile Pro Ala
 65 70 75 80
 Ser Val Arg Tyr Ser Leu Gly Gly Val Ala Met Asp Asp Lys Ser Lys
 85 90 95
 Val Arg Gly Met Ala Leu Lys Leu Glu Asn Gln Asn Ala Ser Trp Thr
 100 105 110
 Met Val Met Leu Asn Thr Glu Ile Asn Phe Ala Lys Asn Pro Glu Glu
 115 120 125
 Phe Ala Gln Phe Phe Glu Met Arg Leu Pro Lys Asn Gly Gln Gly Arg
 130 135 140

(2) INFORMATION FOR SEQ ID NO:1772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...528

SUBSTITUTE SHEET (RULE 26)

1306

275 280 285
 Tyr Lys Glu Leu Lys Gly Tyr Ala Asn Lys Glu Gly Gln Gly Asn Thr
 290 295 300
 Gly Leu
 305

(2) INFORMATION FOR SEQ ID NO:1770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1770

Pro Gln Arg Val Val Phe Arg Val Arg Phe Leu Leu Ala Ile Pro Gln
 1 5 10 15
 Ile Leu Val Gly Leu Arg Ile Ala Val Val Met Leu Val Ala Met Ala
 20 25 30
 Gly Ile Gly Ala Leu Ile Gly Ala Gly Gly Leu Gly Gln Ala Ile Phe
 35 40 45
 Arg Gly Leu Asn Thr Gln Asn Thr Thr Ile Leu Val Ala Gly Ser Phe
 50 55 60
 Ile Ile Ala Leu Phe Ser Val Leu Ala Asp Gln Phe Val Ser Val Phe
 65 70 75 80
 Gln His Glu Asn Ala Leu Gln Arg Leu Phe Ser Gln Asn Ala Thr Gln
 85 90 95
 Lys Gln Lys Arg Arg Val Tyr Val Asn Leu Ala Val Phe Leu Phe Leu
 100 105 110
 Leu Leu Ala Ser Ala Leu Trp Leu Ile Pro Arg Ser Ala Ile Glu Glu
 115 120 125
 Lys Pro Leu Val Val Ala Thr Lys Pro Ser Ser Glu Gln Tyr Ile Leu
 130 135 140
 Gly Glu Ile Leu Ser Leu Leu Leu Glu Lys His His Ile Pro Ile Lys
 145 150 155 160
 Arg Ala Phe Gly Ile Gly Gly Gly Thr Met Asn Ile His Pro Ala Leu
 165 170 175
 Ile Arg Gly Asp Phe Asp Leu Tyr Val Glu Tyr Thr Gly Thr Ala Trp
 180 185 190
 Val Asn Thr Leu Lys Asn Pro Leu Thr Gln Lys Val Asp Phe Glu Thr
 195 200 205
 Ile Lys Lys Arg Tyr Glu Lys Glu Phe Asn Leu Leu Trp Val Gly Leu
 210 215 220
 Leu Gly Phe Asn Asn Thr Tyr Ser Leu Ala Ile Ser Lys Glu Asp Ala
 225 230 235 240
 Gln Lys Tyr Ala Ile Glu Thr Phe Ser Asp Leu Ala Phe His Ser Pro
 245 250 255
 Asn Phe Asp Phe Gly Ala Glu Phe Asp Phe Phe Glu Arg Glu Asp Ala
 260 265 270
 Phe Lys Gly Leu Ile Lys Ala Tyr Arg Phe His Phe Arg Ser Leu His
 275 280 285
 Glu Met Asp Ile Asn Leu Arg Tyr Lys Ser Phe Glu Ser His Lys Ile
 290 295 300

SUBSTITUTE SHEET (RULE 26)

1305

```

Asp Tyr Ser Leu Ser Ser Ala Arg Gln Asn Ala Leu Glu Lys Val Met
65          70          75          80
Glu Ala Phe Lys Gly Asp Arg Ile Glu Ile Lys Ala Gly Glu Leu Lys
          85          90          95
Ala Thr Phe Ile Asp Thr Asp Lys Val Tyr Val Leu Leu Arg Ile Thr
          100          105          110
Lys Lys His Val Ala Leu Met Asn Glu
          115          120

```

(2) INFORMATION FOR SEQ ID NO:1769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1769

```

Gly Leu Ile Met Lys Lys Ile Ile Leu Ala Cys Leu Val Ala Phe Val
1          5          10          15
Gly Ala Asn Leu Ser Ala Glu Pro Lys Trp Tyr Ser Lys Ala Tyr Asn
          20          25          30
Lys Thr Asn Ala Gln Lys Gly Tyr Leu Tyr Gly Ser Gly Ser Ala Thr
          35          40          45
Ser Lys Glu Ala Ser Lys Gln Lys Ala Leu Ala Asp Leu Val Ala Ser
          50          55          60
Ile Ser Val Val Val Asn Ser Gln Ile His Ile Gln Lys Ser Arg Val
65          70          75          80
Asp Asn Lys Leu Lys Ser Ser Asp Ser Gln Thr Ile Asn Leu Lys Thr
          85          90          95
Asp Asp Leu Glu Leu Asn Asn Val Glu Ile Val Asn Gln Glu Ala Gln
          100          105          110
Lys Gly Ile Tyr Tyr Thr Arg Val Arg Ile Asn Gln Asn Leu Phe Leu
          115          120          125
Gln Gly Leu Arg Asp Lys Tyr Asn Ala Leu Tyr Gly Gln Phe Ser Thr
          130          135          140
Leu Met Pro Lys Val Cys Lys Gly Val Phe Tyr Lys Gln Ser Lys Ser
145          150          155          160
Met Gly Asp Leu Leu Ala Lys Ala Ala Pro Met Glu Arg Ile Leu Lys
          165          170          175
Ala Tyr Ser Val Pro Val Ser Ser Leu Glu Asn Tyr Glu Lys Ile Tyr
          180          185          190
Tyr Gln Asn Ala Phe Lys Pro Lys Val Arg Ile Ala Phe Asp Asp Asn
          195          200          205
Ser Asp Thr Glu Ile Lys Asn Ala Leu Met Ser Ala Tyr Ala Arg Val
          210          215          220
Leu Thr Pro Ser Asp Glu Glu Lys Leu Tyr Gln Ile Lys Asn Glu Val
225          230          235          240
Phe Thr Asp Ser Ala Asn Gly Ile Thr Arg Ile Arg Val Ile Ile Ser
          245          250          255
Ala Ser Asp Cys Gln Gly Thr Pro Val Leu Asn Arg Ser Leu Glu Val
          260          265          270
Asp Glu Lys Asn Lys Asn Phe Ala Ile Thr Arg Leu Gln Ser Leu Leu

```

```

      20      25      30
Ile Lys Met Gln Lys Lys Ala Gln Glu Gln Glu Asn Asp Gly Ser Lys
      35      40      45
Arg Pro Ser Tyr Val Asp Ser Asp Tyr Glu Val Phe Ser Glu Thr Ile
      50      55      60
Phe Leu Gln Asn Met Val Tyr Gln Pro Ile Glu Glu Arg Asn Ala Phe
      65      70      75      80
Phe Gln Leu Thr Lys Asp Glu Asp Asn Ser Phe Asn Pro Glu Asn Ser
      85      90      95
Val Ile Leu Leu Asn Glu Pro Ser Asp Asn Ser Glu Lys Asn Leu Leu
      100      105      110
Ser Tyr Pro Asn Asp Pro Asn Asn Asn Glu Asp Asn Ala Asn Asn Ser
      115      120      125
Gln Lys Asn Pro Phe Leu Tyr Lys Pro Lys Arg Lys Thr Lys Asn Pro
      130      135      140
Lys Leu Ile Glu Tyr Ser Gln Gln Asp Phe Tyr Pro Leu Lys Asn Gly
      145      150      155      160
Asp Ile Ile Met Ser Lys Glu Gly Asp Gln Trp Leu Ile Glu Ile Gln
      165      170      175
Ser Lys Ala Leu Lys Arg Phe Leu Lys Asp Gln Asn Asp Lys Asp Arg
      180      185      190
Gln Ile Gln Thr Phe Thr Phe Asn Asp Thr Lys Thr Gln Ile Ala Gln
      195      200      205
Ile Lys Gly Lys Ile Ser Ser Tyr Val Tyr Thr Thr Asn Asn Gly Ser
      210      215      220
Leu Ser Leu Arg Pro Phe Tyr Glu Ser Phe Leu Leu Glu Lys Lys Ser
      225      230      235      240
Asp Asn Val Tyr Thr Ile Glu Asn Lys Ala Leu Asp Thr Met Glu Ile
      245      250      255
Ser Lys Cys Gln Met Val Leu Lys Lys His Ser Thr Asp Lys Leu Asp
      260      265      270
Ser Gln His Lys Ala Ile Ser Ile Asp Leu Asp Phe Lys Lys Glu Arg
      275      280      285
Phe Lys Ser Asp Thr Glu Leu Phe Leu Glu Cys Leu Lys Glu Ser
      290      295      300

```

(2) INFORMATION FOR SEQ ID NO:1768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1768

```

Ala Trp Leu Lys Ser Arg Val Leu Met Lys Arg Leu Ala Val Ala Leu
1      5      10      15
Ile Leu Val Leu Gly Val Val Trp Gly Lys Ser Leu Pro Lys Trp Ala
      20      25      30
Lys Asp Cys Ser Lys Glu Met Arg Ile Glu Lys Thr Gln Thr Lys Asp
      35      40      45
Glu Lys Ile Leu Val Cys Gly Met Ser Asp Ile Leu Leu Ser Asp Met
      50      55      60

```

1303

Ala Asn Glu Asp Leu Lys Arg Gln Asn Arg Lys Leu Glu Glu Glu Asn
 290 295 300
 Ile Ala Leu Lys Glu Arg Val Asp Gly Leu Asn Glu Gln Leu Ser Lys
 305 310 315 320
 Leu Gln Pro Gln Lys Pro Gln
 325

(2) INFORMATION FOR SEQ ID NO:1766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1766

Phe Lys Thr Ile Glu Arg Asn Asp Phe Lys Leu Asn Gly Leu Thr Lys
 1 5 10 15
 Ile Leu Gln Asn Lys Gly Tyr Lys Met Lys Thr Ile Lys Asn Gly Ile
 20 25 30
 Met Ile Gly Thr Leu Gly Ala Leu Leu Leu Ser Gly Cys Ser Ser Phe
 35 40 45
 Asp Ala Gln Arg Phe Ala Cys Leu Pro Lys Asp His Ser Ser Lys Asp
 50 55 60
 Ala Ser Thr Lys Lys Glu Ala Gln Tyr Ile Pro Lys Gly Phe Phe Asp
 65 70 75 80
 Pro Tyr Ser Ser Asn Leu Asn His Trp Asp Ser Thr Phe
 85 90

(2) INFORMATION FOR SEQ ID NO:1767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1767

Ser Leu Asn Lys Gly Leu Ala Leu Phe Leu Val Lys Lys Ile Gly Val
 1 5 10 15
 Val Ile Met Ile Leu Val Cys Phe Leu Ala Cys Ser Gln Glu Ser Phe

1302

```

      85          90          95
Ser Leu Ala Ala Asn Lys Arg Val Phe Ser Leu Ala Lys Met Ser Phe
      100          105          110
Ser Val Phe Ser Ser Ala Phe Ser Leu Val Ser Leu Leu Leu Phe Cys
      115          120          125
His Asn
      130

```

(2) INFORMATION FOR SEQ ID NO:1765:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1765

```

Met Gly Thr Leu Ile Glu Lys Trp Phe Gly Phe Ser Gln Ile Arg Glu
1      5      10      15
Glu Leu Glu Ala Arg Ile Ser Glu Leu Glu Asp Glu Asn Thr Glu Leu
      20      25      30
Leu Arg Glu Arg Glu Tyr Leu Ala Glu Thr Ser Glu Leu Lys Asp
      35      40      45
Ala Asn Asp Gln Leu Arg Gln Lys Asn Asp Lys Leu Phe Ile Thr Lys
      50      55      60
Asp Lys Leu Thr Lys Glu Asn Thr Glu Leu Phe Ala Glu Asn Glu Ser
      65      70      75      80
Leu Ser Val Lys Ile Ser Gly Leu Glu His Ser Asn Asp Gln Leu Trp
      85      90      95
Gln Asn Asn Asn Lys Leu Thr Lys Glu Lys Ala Glu Leu Lys Thr Glu
      100     105     110
Lys Asp Ile Leu Ala Lys Glu Asn Thr Arg Leu Leu Ala Ala Arg Asp
      115     120     125
Arg Leu Thr Glu Glu Lys Arg Glu Leu Thr Thr Glu Lys Glu Arg Leu
      130     135     140
Lys Arg Glu Asn Thr Glu Leu Thr His Lys Ile Thr Glu Leu Thr Lys
      145     150     155     160
Glu Asn Lys Ala Leu Thr Thr Glu Asn Asp Lys Leu Asn His Gln Val
      165     170     175
Thr Ala Leu Thr Asn Glu Arg Asp Ser Leu Glu Gln Glu Arg Ala Arg
      180     185     190
Leu Gln Asp Ala His Gly Phe Leu Glu Lys Arg Cys Thr Asn Leu Glu
      195     200     205
Lys Glu Asn Gln Arg Leu Thr Asp Lys Leu Lys Gln Leu Glu Ser Ala
      210     215     220
Gln Lys Ser Leu Glu Asn Thr Asn Asn Gln Leu Arg Gln Ala Leu Glu
      225     230     235     240
Asn Ser Asn Val Gln Leu Ala Gln Ala Lys Glu Lys Ile Ala Ile Glu
      245     250     255
Lys Ser Glu Leu Glu Arg Glu Ile Ala Arg Leu Lys Ser Leu Glu Gly
      260     265     270
Met Glu Ala Lys Ser Asp Leu Asp Leu His Asn Arg Arg Leu Ala Ser
      275     280     285

```

SUBSTITUTE SHEET (RULE 26)

1301

Leu Glu Asp Leu Lys Leu Glu Asp Phe Glu Pro Leu Arg Lys Leu Ser
 35 40 45
 His Phe Ile Val Ile Gly Asn Leu Phe Gly Lys Ser Ser Asn Asp Thr
 50 55 60
 Gln Glu Asn Pro Lys Asp Ala Leu Lys Ser Thr Asn Phe His Glu Lys
 65 70 75 80
 His Thr Lys Pro Thr Glu Thr Thr Glu Leu Val Glu Glu Asn Lys Ala
 85 90 95
 Leu Thr Thr Glu Lys Glu Arg Leu Glu Arg Glu Asn Lys Asn Leu Thr
 100 105 110
 Ala Asp Lys Glu Asn Leu Thr Lys Glu Lys Thr Glu Leu Lys Gln
 115 120 125
 Val Asn Glu Leu Lys Asn Ser Lys Gln Val Leu Glu Asn Glu Lys Ala
 130 135 140
 Asp Trp Leu Arg Glu Lys Glu Asn Leu Thr Lys Asp Arg Glu Asn Leu
 145 150 155 160
 Thr Lys Glu Lys Thr Glu Leu Thr Glu Lys Asn Lys Val Leu Thr Thr
 165 170 175
 Glu Lys Glu Arg Leu Ala Thr Glu Lys Glu Asn Leu Thr Lys Glu Lys
 180 185 190
 Thr Glu Ser Gln Lys Gln Val Asn Glu Leu Lys Asn Ser Lys Gln Val
 195 200 205
 Leu Glu Asn Glu Lys Ala Asp Leu Thr Asn Glu Asn Thr Lys Leu Lys
 210 215 220
 Thr Asp Lys Thr Asp Leu Thr Glu Lys Asn Gln Arg Leu Thr Thr Glu
 225 230 235 240
 Lys Thr Glu Leu Asn Asn Lys Ile Thr Gly Leu Ala Thr Glu Lys Glu
 245 250 255
 Arg Leu Ala Ala Asp Lys Glu Asn Leu Thr Lys Glu Ser Arg Gln Arg
 260 265 270
 Lys Pro Asn
 275

(2) INFORMATION FOR SEQ ID NO:1764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1764

Ala Leu Ser Asn Cys Leu Ser Leu Ser Val Arg Arg Trp Phe Ser Phe
 1 5 10 15
 Ser Lys Leu Val His Arg Phe Ser Arg Asn Pro Cys Ala Ser Cys Asn
 20 25 30
 Arg Ala Arg Ser Cys Ser Arg Leu Ser Arg Ser Leu Val Ser Ala Val
 35 40 45
 Thr Trp Trp Leu Ser Leu Ser Phe Ser Val Val Ser Ala Leu Phe Ser
 50 55 60
 Leu Val Ser Ser Val Ile Leu Trp Val Ser Ser Val Phe Ser Leu Phe
 65 70 75 80
 Ser Leu Ser Phe Ser Val Val Asn Ser Leu Phe Ser Ser Val Ser Arg

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1300

Gly Leu 340 345 350

(2) INFORMATION FOR SEQ ID NO:1762:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1762

Met	Gln	Lys	Phe	Phe	Ser	Arg	Phe	Arg	Arg	Trp	Ala	Leu	Pro	Phe	Tyr
1				5				10						15	
Phe	Val	Ser	Ala	Leu	Ala	Ala	Ile	Asp	Ile	Asp	Glu	Val	Thr	Glu	Ala
			20					25					30		
Gln	Ala	Asn	Ser	Ile	Lys	Leu	Ser	Asp	Gln	Leu	Val	Ser	Leu	Ser	Asp
		35					40					45			
Lys	Leu	Leu	Glu	Lys	Ala	Val	Asp	Arg	Gly	Arg	Asn	Thr	Asp	His	Leu
		50				55					60				
Lys	Asp	Leu	Asn	Asp	Leu	His	Glu	Lys	Ile	Lys	His	Leu	Arg	Leu	Ile
65				70					75					80	
Leu	Glu	Pro	Lys	Pro	Lys	Gly	Lys	Glu	Asp	Ser	Pro	Asn	Leu	Gly	Gly
			85					90						95	
Asn	Lys	Asp	Met	Lys	Thr	Val	Glu	Ile	Gly	Ser					
			100					105							

(2) INFORMATION FOR SEQ ID NO:1763:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1763

Lys	Asn	Gln	Ile	Leu	Gln	Ile	Pro	Leu	Leu	Pro	Pro	Pro	Pro	Asn	Asn
1				5				10						15	
Glu	Glu	Leu	Leu	Lys	Ser	Ile	Thr	Asp	Leu	Lys	Asp	Arg	Leu	Lys	Lys
			20					25						30	

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(2) INFORMATION FOR SEQ ID NO:1761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1761

```

Arg Gly Val Ser Ile Lys Glu Glu Ser Gln Thr Leu Ala Asp Ile Thr
1      5      10      15
Phe Gln Asn Tyr Phe Arg Met Phe Ser Lys Leu Ser Gly Met Thr Gly
20      25      30
Thr Ala Gln Thr Glu Ala Thr Glu Phe Leu Glu Ile Tyr Asn Leu Glu
35      40      45
Val Val Ser Ile Pro Thr Asn Leu Ala Ile Lys Arg Lys Asp Leu Asn
50      55      60
Asp Leu Ile Tyr Lys Ser Glu Lys Glu Lys Phe Asp Ala Val Ile Leu
65      70      75      80
Lys Ile Lys Glu Leu His Asp Lys Gly Gln Pro Val Leu Val Gly Thr
85      90      95
Ala Ser Ile Glu Lys Ser Glu Thr Leu His Ala Leu Leu Lys Lys Glu
100     105     110
Arg Ile Pro His Thr Val Leu Asn Ala Lys Gln His Thr Lys Glu Ala
115     120     125
Glu Ile Ile Lys Asp Ala Gly Leu Lys Gly Ala Val Thr Ile Ala Thr
130     135     140
Asn Met Ala Gly Arg Gly Val Asp Ile Lys Leu Thr Asp Glu Val Lys
145     150     155     160
Glu Leu Gly Gly Leu Tyr Ile Ile Gly Thr Glu Arg His Glu Ser Arg
165     170     175
Arg Ile Asp Asn Gln Leu Arg Gly Arg Ser Gly Arg Gln Gly Asp Pro
180     185     190
Gly Val Ser Gln Phe Tyr Leu Ser Leu Glu Asp Asn Leu Leu Arg Ile
195     200     205
Phe Gly Ser Asp Arg Thr Lys Gly Val Met Glu Lys Leu Gly Pro Lys
210     215     220
Asp Gly Glu His Ile Glu Phe Lys Leu Val Thr Arg Ala Val Glu Asn
225     230     235     240
Ala Gln Lys Lys Val Glu Asn Leu His Phe Asp Ser Arg Lys His Leu
245     250     255
Leu Glu Tyr Asp Asp Val Ala Asn Glu Gln Arg Thr Ser Val Tyr Asn
260     265     270
Leu Arg Asp Glu Leu Leu Asp Ile Asn Tyr Asp Ile Ser Ala Lys Ile
275     280     285
Ala Glu Asn Arg Glu Tyr Ala Leu Asn Gln Ile Phe Ser Lys Leu Lys
290     295     300
Ala Phe Asp His Gln Asn Leu Ser Glu Glu Glu Leu Leu Gly Leu Lys
305     310     315     320
Asn Ile Leu Lys Glu Asp Phe Asn Ala Ser Val Glu Leu Glu Asp Leu
325     330     335
Glu Lys Ala Ser Pro Ile Glu Ile Phe Val Ala Glu Lys Leu Lys Ser

```

SUBSTITUTE SHEET (RULE 26)

1298

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...365

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1760

```

Lys Leu Phe Leu Lys Pro Leu Lys Glu Thr Ser Leu Ala Leu Val Gly
1      5      10      15
Val Ala Lys Asn Ile Lys Ile Val Ala Leu Lys Ala Gly Leu Lys Arg
20      25      30
Ala Tyr Leu Pro Asn Arg Ser Leu Ile Phe Phe Leu Ile Lys Arg Tyr
35      40      45
Leu Arg Phe Asp Lys Ser Gln Pro Phe Ile Ser Ile Thr Ala Leu Leu
50      55      60
Ala Phe Phe Gly Val Ala Val Gly Val Met Val Leu Ile Val Ala Met
65      70      75      80
Ala Ile Met Asn Gly Met Ser Lys Glu Phe Glu Lys Lys Leu Phe Val
85      90      95
Met Asn Tyr Pro Leu Thr Leu Tyr Thr Thr Ser Pro Tyr Gly Ile Ser
100      105      110
Glu Glu Val Val Gln Ala Leu Glu Lys Lys Phe Pro Asn Leu Leu Phe
115      120      125
Ser Pro Tyr Leu Gln Thr Gln Ser Pro Ile Lys Ser Ala His Ser Met
130      135      140
Asn Gly Gly Val Val Phe Gly Val Asp Phe Ser Lys Glu Arg His Ile
145      150      155      160
Asn Glu Val Leu Asn Asp Ala Leu Lys Asn Ile Asn Glu Asn Asp Leu
165      170      175
Phe Lys Asn Pro Phe Asn Leu Ile Val Gly Lys Ser Leu Arg Tyr Ser
180      185      190
Leu Asn Leu Asp Leu Asn Gln Lys Ala Asp Leu Phe Phe Thr Glu Leu
195      200      205
Glu Pro Thr Gly Leu Thr Leu Ser Pro Ile Met Lys Arg Phe Thr Ile
210      215      220
Lys Gly Asp Phe Asp Ser Gly Leu Lys Ser Tyr Asp Met Ser Tyr Met
225      230      235      240
Tyr Ala Ser Leu Gln Ala Ile Ser Ala Ile Arg Arg Leu Pro Leu Gly
245      250      255
Leu Tyr Asp Gly Val His Val Tyr Ser Lys Thr Pro Met Lys Asp Ile
260      265      270
Glu Lys Leu Arg Asn Ala Leu Lys Thr Ile Asn His His Gly Ile Gly
275      280      285
Ile Glu Gly Trp Trp Gln Gln Asn Gly Asn Phe Phe Ser Ala Met Glu
290      295      300
Leu Glu Lys Arg Ala Leu Phe Ile Val Leu Met Leu Ile Ile Leu Met
305      310      315      320
Ala Ser Leu Asn Ile Ile Ser Ser Leu Leu Met Val Val Met Asn Arg
325      330      335
Arg Lys Glu Ile Ala Leu Leu Phe Ser Met Gly Ser Ser Gln Lys Glu
340      345      350
Ile Gln Lys Thr Phe Phe Tyr Leu Gly Asn Ile Ile Ser
355      360      365

```

SUBSTITUTE SHEET (RULE 26)

1297

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...356

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1759

```

Lys Val Thr Thr Thr Met Ile Lys Ala Ile Ile Gly Lys Ile Ile Gly
1      5      10      15
Thr Arg Asn Asp Arg Trp Ile Lys Gln Tyr Lys Lys Lys Val Leu Ala
20      25      30
Ile Asn Ala Leu Glu Pro Thr Tyr Glu Lys Met Ser Asp Val Glu Leu
35      40      45
Gln Asn Ala Phe Glu Glu Leu Lys Lys Arg Val Arg Ser Val Glu Lys
50      55      60
Asp Leu Gln Glu Lys Thr Leu Leu Glu Val Leu Pro Glu Ser Phe Ala
65      70      75      80
Ile Thr Arg Glu Ala Ser Lys Arg Ile Leu Lys Met Arg His Phe Asp
85      90      95
Val Gln Leu Ile Gly Gly Met Val Leu Asn Asp Gly Lys Ile Ala Glu
100     105     110
Met Lys Thr Gly Glu Gly Lys Thr Leu Val Ala Thr Leu Ala Val Ala
115     120     125
Leu Asn Ala Met Lys Gly Glu Ser Val Tyr Val Val Thr Val Asn Asp
130     135     140
Tyr Leu Ala His Arg Asp Ser Lys Glu Met Glu Pro Leu Tyr Gln Phe
145     150     155     160
Leu Gly Tyr Ser Val Gly Thr Ile Thr Ala Ser Val Arg Asp Asp Asp
165     170     175
Glu Arg Leu Glu Ile Tyr Ser Lys Asp Ile Val Tyr Gly Thr Asn Asn
180     185     190
Glu Phe Gly Phe Asp Tyr Leu Arg Asp Asn Met Lys Tyr Ser Leu Glu
195     200     205
His Lys Val Gln Lys Ser His Ala Phe Ala Ile Val Asp Glu Val Asp
210     215     220
Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser Gly Pro
225     230     235     240
Val Asp Arg Arg Met Glu Asn Tyr Asn Lys Ala Asp Glu Val Ala Lys
245     250     255
Ser Met Gln Val Glu Val Asp Phe Thr Ile Asp Glu Lys Asn Arg Ala
260     265     270
Ile Leu Ile Thr Glu Glu Gly Ile Lys Lys Ala Glu Asn Leu Phe Gly
275     280     285
Val Asp Asn Leu Tyr Lys Ile Glu Asn Ala Ala Leu Ser His His Leu
290     295     300
Asp Gln Ala Leu Lys Ala Asn Tyr Leu Phe Phe Ile Asp Lys Asp Tyr
305     310     315     320
Ile Val Ala Asn Asn Glu Val Val Ile Val Asp Glu Phe Thr Gly Arg
325     330     335
Leu Ser Glu Gly Arg Arg Phe Ser Glu Gly Leu His Gln Ala Leu Glu
340     345     350
Ala Lys Glu Ala
355

```

(2) INFORMATION FOR SEQ ID NO:1760:

SUBSTITUTE SHEET (RULE 26)

1296

```

370          375          380
Thr Ile Asn Pro Met Phe Leu Asp Lys Glu Arg Ala Lys Glu Arg Phe
385          390          395          400
Trp Asn Thr Gln Tyr Phe Glu Gly Lys Arg Asp Phe Ile Tyr Arg Leu
          405          410          415
Leu Phe Tyr Tyr Ala Pro Phe Lys Val Leu Asp Ser Lys Glu Thr Leu
          420          425          430
Gly Val Ile Glu Glu Gly Leu Phe Leu Leu Asp Ser Asp Thr Gln Lys
          435          440          445
Asp Leu Glu Gly Ala Ser Leu Ala Phe Lys Arg Gly Arg Leu Met Ala
          450          455          460
Ile Ala Asp Lys Asn Ala Leu Lys Gly Leu Lys Glu Leu Glu Lys Lys
          465          470          475          480
Arg Leu Lys Lys Ala Leu Ser Phe Phe Asp Leu Ser Leu Lys Asn Ser
          485          490          495
Pro Asn Asn Ala Leu Leu His Tyr Asn Val Gly Leu Ile Tyr Ala Gln
          500          505          510
Leu Glu Asn Tyr His Lys Ala Tyr Phe His Phe Leu Arg Ala Phe His
          515          520          525
Leu Asn Ser Ala Asp Tyr Leu Ser Ala Val Phe Ala Val Leu Ala Ser
          530          535          540
His Phe Thr His Glu Asp Thr Thr Glu Phe Leu Arg Glu Ile Thr Glu
          545          550          555          560
Asn Phe Tyr Ser His Asp Phe Ser Ser Pro Thr Gln Lys Ala Leu Leu
          565          570          575
Ser Ser Leu Ile Ala Tyr Leu Asn Tyr Arg Thr Asn Trp Asp Met Asp
          580          585          590
Trp Leu Lys Asn Ala Pro Lys Lys Leu Pro Phe Tyr Tyr Ala Leu Glu
          595          600          605
Ala Val Phe Ala Lys Glu Ser Lys Asp Lys Lys Leu Met Val Gln Ser
          610          615          620
Phe Gly Asn Leu Lys Lys Met Leu Pro Lys Asp Leu Ile Ser Asn Ile
          625          630          635          640
Phe Tyr Glu Ile Val Ser Tyr Tyr Asp Ala Ser Ile Arg His Thr Leu
          645          650          655
Ser Ile Tyr Thr Leu Leu Asp Ser His Lys Ile Ser Trp Asp Gln Thr
          660          665          670
Met Gln Gly Pro Ile Leu Gly Arg His Phe Tyr Thr Tyr Met Gly Phe
          675          680          685
Met Val Asn Asp Leu Asp His Gln Glu Arg Leu Leu Glu Gln Lys Ile
          690          695          700
Ala Ser Leu Glu Arg Gly Glu Ala Pro Asn Asp Trp Leu Glu Asn Leu
          705          710          715          720
Ala Leu Val Ser Leu Phe Gln Gly Gln Tyr Glu Lys Ala Ser Ala Leu
          725          730          735
Tyr Gln Asn Leu Ile Asp Gly Leu Lys Asp Asn Glu Ala Arg Leu Lys
          740          745          750
Ile Leu Ala Gly Leu Thr Tyr Ile Ala Gln Asn Asn Tyr Asn Asn Ala
          755          760          765
Ala Leu Trp Leu Glu Leu Gly Lys Leu Asp Asp Pro Asn Asn Glu Asn
          770          775          780
Ile Arg Tyr Ala Leu Gly Leu Leu Tyr Gln Arg Lys Gly Asp Leu Lys
          785          790          795          800
Ser Ala Leu Asn His Phe Leu Ala Ile Lys Thr Ser Asp Phe Ser Ser
          805          810          815
Pro Tyr Phe Asp Phe Glu Ile Asp Thr Asn Leu Leu Lys Glu Arg Leu
          820          825          830
Asn Gln Glu Glu Lys Gly Glu Phe Leu Glu
          835          840

```

(2) INFORMATION FOR SEQ ID NO:1759:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 356 amino acids

SUBSTITUTE SHEET (RULE 26)

1295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 842 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1758

```

Phe Val Leu Asn Glu Glu Gln Asn Ser Leu Glu Glu Lys Gly Gly Glu
1          5          10          15
Asn Lys Asn Glu Lys Glu Thr Pro Leu Lys Gly Ile His Ser Lys Ile
20          25          30
Pro Ser Leu Lys Gln Ala Leu Glu Gln Thr Ile Ser Lys Ile Lys Ser
35          40          45
Ser Lys Glu Phe Phe Lys Gln Leu Leu His Asn Lys Lys Lys Leu Tyr
50          55          60
Ile Ala Leu Gly Ile Leu Leu Ser Leu Ile Ala Leu Ile Val Ala Leu
65          70          75          80
Ser Leu Leu Leu Gly His Lys Lys Glu Asn Lys Gln Thr Ser Leu Gln
85          90          95
Thr Asn Thr Ala Thr Thr Asn Asn Glu Thr Pro Asn Asp Thr Asn Asn
100         105         110
Ala Glu Ala Glu Gly Gln Ile Glu Asn Leu Asp Leu Pro Asp Leu Ile
115         120         125
Gly Lys Asp Ser Leu Lys Arg Asn Asp Glu Ser Gln Val Asp Ala Met
130         135         140
Met Gln Lys Ala Ser Leu Leu Tyr Glu Gln Gly Gln Lys Asp Glu Ala
145         150         155         160
Leu His Leu Phe Asp Lys Ile Ala Ser Phe Ser Gln Gly Ile Ala Ser
165         170         175
His Asn Leu Gly Val Ile Lys Phe Lys Glu Lys Asp Phe Asn Gly Ala
180         185         190
Leu Asp Leu Phe Asp Ser Ser Ile Ala Ser Lys Glu Asn Ala Ser Val
195         200         205
Ser Ala Ile Asp Ala Leu Val Thr Ala Tyr His Leu Gln Asp Ala Asp
210         215         220
Leu Tyr Tyr His Tyr Leu Lys Ile Val Arg Asp Thr Leu Tyr Lys Asp
225         230         235         240
Tyr Lys Lys Ser Phe Tyr Ser Tyr Ala Tyr Ala Leu Lys Ser Tyr Tyr
245         250         255
Ala Gly Glu Tyr Phe Glu Ala Leu Ser Pro Leu Met His Pro Asn Ser
260         265         270
Asn Ala Phe Leu Lys Pro Asn Ala Arg Leu Ala Ser Lys Leu Phe Leu
275         280         285
Met Phe Lys Asp Glu Thr Asn Ala Tyr Lys Gln Leu Gln Lys Ser Ala
290         295         300
Asn Ala Gln Asp Glu Leu Ala Leu Gly Leu Leu Gln Ala Arg Leu Gly
305         310         315         320
Thr Tyr Lys Gln Ala Leu Glu His Leu Gln His Tyr Leu His Asn Tyr
325         330         335
Pro Lys Asp Leu Asn Ala Leu Met Ala Leu Glu Leu Val Ser Leu Lys
340         345         350
Met Gly Asp Thr Leu Lys Ala Ser Glu Ala Leu Lys Leu Ala Ser His
355         360         365
Thr Gln Glu Asp Thr Leu Leu Ala Asn Ser Phe Tyr Pro Ile Lys Pro

```

SUBSTITUTE SHEET (RULE 26)

1294

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1757

```

His Gln Ser Phe Lys Arg Ala Phe Glu Pro Arg Arg Lys Gly Arg Val
1      5      10      15
Phe Arg Ile Met Gly Phe Glu Lys Ser Ile Leu Asp Asn Leu Asn Gly
20      25      30
Ala Gln Lys Ile Ala Ala Cys His Ile Gln Gly Pro Leu Leu Ile Leu
35      40      45
Ala Gly Ala Gly Ser Gly Lys Thr Lys Thr Leu Thr Ser Arg Leu Ala
50      55      60
Tyr Leu Ile Gly Ala Cys Gly Val Pro Ser Glu Asn Thr Leu Thr Leu
65      70      75      80
Thr Phe Thr Asn Lys Ala Ser Lys Glu Met Gln Glu Arg Ala Leu Lys
85      90      95
Leu Leu Lys Asn Gln Ala Leu Ile Pro Pro Leu Leu Cys Thr Phe His
100      105      110
Arg Phe Gly Leu Leu Phe Leu Arg Gln His Met Asn Leu Leu Lys Arg
115      120      125
Ala Cys Asp Phe Ser Val Leu Asp Ser Asp Glu Val Lys Thr Leu Cys
130      135      140
Lys Gln Leu Lys Ile Ser Asn Phe Arg Ala Ser Ile Ser Gln Ile Lys
145      150      155      160
Asn Gly Met Met Asp Leu Ser Val Gln Asp Ser Glu Cys Tyr Lys Ala
165      170      175
Tyr Glu Leu Tyr Gln Asn Ala Leu Lys Lys Asp Asn Leu Val Asp Phe
180      185      190
Asp Asp Leu Leu Cys Leu Ser Leu Lys Ile Leu Gln Asp Asn Glu Lys
195      200      205
Leu Ala Lys Glu Thr Ser Glu Arg Tyr His Tyr Ile Met Val Asp Glu
210      215      220
Tyr Gln Asp Thr Asn Ala Leu Gln Leu Glu Phe Leu Lys Gln Leu Ser
225      230      235      240
Phe Thr His His Asn Leu Cys Val Val Gly Asp Asp Asp Gln Ser Ile
245      250      255
Tyr Gly Phe Arg Gly Ala Asp Ile Ser Asn Ile Leu Asn Phe Ser Lys
260      265      270
His Phe Lys Gly Ala Lys Ile Val Lys Leu Glu Thr Asn Tyr Arg Ser
275      280      285
Ser Ala Glu Ile Leu Ala Cys Ala Asn Ser Leu Ile Ser His Asn Gln
290      295      300
His Arg His Ile Lys Thr Leu Gln Ser Phe Lys Gly Ser His Lys Ser
305      310      315      320
Val Ile Cys Lys Glu Tyr Pro Thr Gln Lys Glu Glu Ser Leu Asp Val
325      330      335
Ala Tyr Gln Ile Gln Ser Pro Phe Lys Glu Gly Arg Glu Phe Arg Lys
340      345      350
Tyr Arg Tyr Phe Val Ser Phe Lys Trp
355      360

```

(2) INFORMATION FOR SEQ ID NO:1758:

SUBSTITUTE SHEET (RULE 26)

1293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1755

```

His Asn Lys Thr Arg Met Lys Arg Ala Lys Arg Arg Lys Phe Ile Thr
1      5      10      15
Lys Phe Ser Arg Tyr Tyr Thr Pro Ser Val Leu Phe Ile Ala Leu Met
      20      25      30
Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu Trp
      35      40      45
Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala Leu
      50      55      60
Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala Ser
65      70      75      80
Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Val Leu Thr
      85      90      95
Gln Thr Lys Ser Ile Ala Phe Asp Lys Thr Gly Thr Leu Thr Lys Gly
      100     105     110
Val Phe Lys Val Val Asp Ile Val Pro Gln Asn Gly His Ser Lys Glu
      115     120     125
Glu Val Cys Ile Thr Leu Leu Ala Arg Ser Phe Tyr Pro Arg Thr Arg
130     135     140
Ser Leu Tyr Pro Phe Lys Lys His Ala Lys Lys Cys
145     150     155

```

(2) INFORMATION FOR SEQ ID NO:1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1756

```

Arg Ser Thr Leu Ala Ser Ala Asp Val Gly Ile Gly Met Gly Lys Gly
1      5      10      15
Ser Glu Leu Ser Lys Gln Ser Ala Asp Ile Val Ile Thr Asn Asp Ser
      20      25      30
Leu Ser Ser Leu Val Lys Val Leu Ala Ile Ala Lys Lys Thr Lys Ser
      35      40      45
Ile Ile Trp Gln Asn Ile Leu Phe Ala Leu Gly Ile Lys Ala Val Phe
      50      55      60
Ile Val Leu Gly Leu Met Gly Val Ala Ser Leu Trp Glu Ala Val Phe
65      70      75      80
Gly Asp Val Gly Val Thr Leu Leu Asp Leu Ala Asn Ser Met Arg Thr
      85      90      95
Met Arg Ala

```

(2) INFORMATION FOR SEQ ID NO:1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids
 (B) TYPE: amino acid

1292

145		150		155		160									
Val	Val	Met	Leu	Lys	Asp	Lys	Lys	Leu	Phe	Leu	Gln	Ala	Ser	Thr	Pro
		165		170		175									
Ile	Ala	Met	Thr	Ser	His	Asn	Leu	Ser	Ala	Leu	Tyr	Asp	Thr	Pro	Leu
		180		185		190									
Glu	Ala	Ile	Trp	His	Asp	Asp	Lys	Leu	Val	Val	Tyr	Ala	Leu		
		195		200		205									

(2) INFORMATION FOR SEQ ID NO:1754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1754

Lys	Lys	Lys	Lys	Asn	Asp	Glu	Lys	His	Ile	Ala	Lys	His	Phe	Val	Ala
1				5					10					15	
Val	Ser	Thr	Asn	Lys	Glu	Ala	Val	Gln	Gln	Phe	Gly	Ile	Asp	Glu	His
			20					25					30		
Asn	Met	Phe	Gly	Phe	Trp	Asp	Phe	Val	Gly	Gly	Arg	Tyr	Ser	Leu	Trp
		35				40					45				
Ser	Ala	Ile	Gly	Leu	Ser	Ile	Met	Ile	Tyr	Leu	Gly	Lys	Lys	Asn	Phe
		50				55				60					
Asn	Ala	Leu	Leu	Lys	Gly	Ala	Tyr	Leu	Met	Asp	Glu	His	Phe	Arg	Asn
				70					75					80	
Ala	Pro	Phe	Glu	Ser	Asn	Leu	Pro	Val	Leu	Met	Gly	Leu	Ile	Gly	Val
			85						90					95	
Trp	Tyr	Ile	Asn	Phe	Phe	Gln	Ser	Lys	Gly	His	Leu	Ile	Ala	Pro	Tyr
			100					105						110	
Asp															

(2) INFORMATION FOR SEQ ID NO:1755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...156

1291

(B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1752

```

Lys Gly Lys Leu Gly Leu Phe Tyr Tyr Phe Ser Asp Leu Leu Glu Ser
1      5      10      15
Leu Ile Cys Phe Ser Asn Ser Cys Cys Lys Ala Cys Cys Cys Phe Ser
      20      25      30
Phe Phe Glu Arg Arg Arg Phe Phe Leu Gly Phe Phe Ser Phe Phe Glu
      35      40      45
Glu Val Ser Gly Ser Phe Glu Ala Val Ser Leu Ser Val Leu Ala Leu
      50      55      60
Val Ile Gly Ser Arg Ser Gly Leu Glu Glu Phe Cys Val Leu Glu Glu
      65      70      75      80
Leu Ile Asn Ser Gly Leu Ser Val Trp Leu Ser Ser Ser Pro Leu Leu
      85      90      95
Leu Phe Trp Asn Ala Ala Leu Val Ser Phe Ser Ala Cys Ser Ser Ile
      100     105     110
Phe Leu Arg Thr Ile Ala Ser Thr Phe Leu Ala Phe Ser Phe Trp Leu
      115     120     125
Thr Leu Thr Met Leu Ile Lys Tyr Leu Ile Tyr Pro Ser Tyr Met Ser
      130     135     140
Pro Asn Cys Ser Cys Lys Ala Pro Lys Ser Glu Pro Leu
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:1753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1753

```

Gly Leu Leu Lys Pro Leu Glu Glu Thr Glu Ile Lys Ala Cys Asn Lys
1      5      10      15
Asp Ile Leu Pro Leu Lys Pro Tyr Glu Lys Ala Lys Leu Ile Ala Tyr
      20      25      30
Ile Pro Gln Val Glu Tyr Tyr Ala Phe Asn Phe Ser Val Leu Asp Phe
      35      40      45
Val Leu Met Gly Lys Ala Thr His Leu Asn Leu Phe Ala Met Pro Lys
      50      55      60
Ala Lys His Ile Lys Glu Ala Thr Ser Val Leu Glu Arg Leu Asp Leu
      65      70      75      80
Glu Ser Leu Lys Asp Gln Gly Ile Asn Asp Leu Ser Gly Gly Gln Arg
      85      90      95
Gln Met Val Leu Leu Ala Arg Ser Leu Leu Gln Arg Thr Pro Leu Leu
      100     105     110
Leu Leu Asp Glu Pro Thr Ser Ala Leu Asp Leu Lys Asn Gln Ala Leu
      115     120     125
Phe Phe Asp Ala Ile Lys Asp Glu Met Lys Lys Arg Glu Leu Ser Val
      130     135     140
Leu Val Asn Ile His Asp Pro Asn Leu Val Ala Arg His Ser Thr His

```

1290

```

145          150          155          160
Asp Gly Val Phe Asp Glu Leu Tyr Lys Asn Ile Leu Lys Gln Ser
          165          170          175
His Tyr Arg Pro Lys His Phe Glu Glu Ser Val Glu Arg Leu Leu Ile
          180          185          190
Leu Gln Lys Ile Ser Ala Leu Phe Pro Lys Thr Thr Thr Pro Leu Glu
          195          200          205
Gln Ser Ser Leu Ser Leu Trp Ala Lys Leu Gln Asp Lys Leu Asp Ile
          210          215          220
Leu Ile Leu Asn Pro Asn Asp Val Lys Ile Ser Leu Asn Glu Glu Glu
225          230          235          240
Met Lys Lys Tyr Tyr Glu Asn His Arg Lys Asp Phe Lys Lys Pro Thr
          245          250          255
Ser Phe Lys Thr Arg Ser Leu Tyr Phe Asp Ala Ser Leu Glu Lys Thr
          260          265          270
Asp Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser Tyr
          275          280          285
Leu Asp Lys Glu Gly Lys Leu Gln Asp Phe Lys Ser Val Gln Glu Gln
          290          295          300
Val Lys His Asp Leu Asn Met Gln Lys Ala Asn Glu Lys Ala Leu Arg
305          310          315          320
Ser Tyr Ile Ala Leu Lys Lys Gly Asn Ala Gln Asn Tyr Thr Thr Gln
          325          330          335
Asp Phe Glu Lys Asn Asn Ser Pro Tyr Thr Ala Glu Ile Thr Gln Lys
          340          345          350
Leu Thr Ala Leu Lys Pro Leu Glu Val Leu Lys Pro Glu Pro Phe Lys
          355          360          365
Asp Gly Phe Ile Val Val Gln Leu Val Ser Gln Ile Lys Asp Glu Leu
          370          375          380
Gln Asn Phe Asp Glu Ala Lys Ser Ala Leu Lys Thr Arg Leu Thr Gln
          385          390          395          400
Glu Lys Thr Leu Met Ala Leu Gln Thr Leu Ala Lys Glu Lys Leu Lys
          405          410          415
Asp Phe Lys Gly Lys Ser Val Gly Tyr Val Ser Pro Asn Phe Gly Gly
          420          425          430
Thr Ile Ser Glu Leu Asn Gln Glu Glu Ser Ala Lys Phe Ile Asn Thr
          435          440          445
Leu Phe Asn Arg Gln Glu Lys Lys Gly Phe Val Thr Ile Gly Asn Lys
          450          455          460
Val Val Leu Tyr Gln Ile Thr Glu Gln Asn Phe Asn His Pro Phe Ser
          465          470          475          480
Ala Glu Glu Asn Gln Tyr Met Gln Arg Leu Val Asn Asn Thr Lys Thr
          485          490          495
Asp Phe Phe Asp Lys Ala Leu Ile Glu Glu Leu Lys Lys Arg Tyr Lys
          500          505          510
Ile Val Lys Tyr Ile Gln
          515

```

(2) INFORMATION FOR SEQ ID NO:1752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

1289

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1750

```

Asn Asn Ala Lys Asn Lys Asn Lys Gly Val Lys Ser Met Lys Thr Asn
1      5      10      15
Phe Tyr Lys Ile Lys Leu Leu Phe Ala Trp Cys Leu Ile Ile Gly Met
20      25      30
Phe Asn Ala Pro Leu Asn Ala Asp Gln Asn Thr Asp Ile Lys Asp Ile
35      40      45
Ser Pro Glu Asp Met Ala Leu Asn Ser Val Gly Leu Val Ser Arg Asp
50      55      60
Gln Leu Lys Ile Glu Ile Pro Lys Glu Thr Leu Glu Gln Lys Val Ala
65      70      75      80
Ile Leu Asn Asp Tyr Asn Asp Lys Asn Val Asn Ile Lys Phe Asp Asp
85      90      95
Ile Ser Leu Gly Ser Phe Gln Pro Asn Asp Asn Leu Gly Ile Asn Ala
100      105      110
Met Trp Gly Ile Gln Asn Leu Leu Met Ser Gln Met Met Ser Asn Tyr
115      120      125
Gly Pro Asn Asn Ser Phe Met Tyr Gly Tyr Ala Pro Thr Tyr Ser Asp
130      135      140
Ser Ser Phe Leu Pro Pro Ile Leu Gly Tyr
145      150

```

(2) INFORMATION FOR SEQ ID NO:1751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 518 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1751

```

Pro Leu Val Lys Ile Arg Leu Phe Asp Phe Thr Ile Arg Leu Phe Lys
1      5      10      15
Pro Glu Phe His Ile Phe Asp Phe Leu Lys Gly Ile Arg Val Leu Met
20      25      30
Ile Glu Trp Met Gln Asn His Arg Lys Tyr Leu Val Val Thr Ile Trp
35      40      45
Ile Ser Thr Ile Ala Phe Ile Ala Ala Gly Met Ile Gly Trp Gly Gln
50      55      60
Tyr Ser Phe Ser Leu Asp Ser Asp Ser Ala Ala Lys Val Gly Gln Ile
65      70      75      80
Lys Ile Ser Gln Glu Glu Leu Ala Gln Glu Tyr Arg Arg Leu Lys Asp
85      90      95
Ala Tyr Ala Glu Ser Ile Pro Asp Phe Lys Glu Leu Thr Glu Asp Gln
100      105      110
Ile Lys Ala Met His Leu Glu Lys Ser Ala Leu Asp Ser Leu Ile Asn
115      120      125
Gln Ala Leu Leu Arg Asn Phe Ala Leu Asp Leu Gly Leu Gly Ala Thr
130      135      140
Lys Gln Glu Val Ala Lys Glu Ile Arg Lys Thr Asn Val Phe Gln Lys

```

SUBSTITUTE SHEET (RULE 26)

1288

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1749

```

Ala Leu Ser Leu Ala Ser Ile Leu Ala Arg Val Glu Glu Leu Ala Lys
1      5      10      15
Leu Ile Asn Asn Asn Asn Asn Lys Lys Leu Arg Gly Phe Phe Leu
20      25      30
Lys Val Leu Leu Ser Leu Val Val Phe Ser Ser Tyr Gly Ser Ala Asn
35      40      45
Asp Asp Lys Glu Ala Lys Lys Glu Ala Leu Glu Lys Glu Lys Asn Thr
50      55      60
Pro Asn Gly Leu Val Tyr Thr Asn Leu Asp Phe Asp Ser Phe Lys Ala
65      70      75      80
Thr Ile Lys Asn Leu Lys Asp Lys Lys Val Thr Phe Lys Glu Val Asn
85      90      95
Pro Asp Ile Ile Lys Asp Glu Val Phe Asp Phe Val Ile Val Asn Arg
100     105     110
Val Leu Lys Lys Ile Lys Asp Leu Lys His Tyr Asp Pro Val Ile Glu
115     120     125
Lys Ile Phe Asp Glu Lys Gly Lys Glu Met Gly Leu Asn Val Glu Leu
130     135     140
Gln Ile Asn Pro Glu Val Lys Asp Phe Phe Thr Phe Lys Ser Ile Ser
145     150     155     160
Thr Thr Asn Lys Gln Arg Cys Phe Leu Ser Leu His Gly Glu Thr Arg
165     170     175
Glu Ile Leu Cys Asp Asp Lys Leu Tyr Asn Val Leu Leu Ala Val Phe
180     185     190
Asn Ser Tyr Asp Pro Asn Asp Leu Leu Lys His Ile Ser Thr Ile Glu
195     200     205
Ser Leu Lys Lys Ile Phe Tyr Thr Ile Thr Cys Glu Ala Val Tyr Leu
210     215     220

```

(2) INFORMATION FOR SEQ ID NO:1750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

1287

Ala Ile Ala Tyr Ala Gln Asn Leu Lys Gly Ile Lys Arg Glu Leu Ser
 690 695 700
 Asp Lys Leu Glu Asn Ile Asn Lys Asp Leu Lys Asp Phe Ser Lys Ser
 705 710 715 720
 Phe Asp Glu Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Ala Glu
 725 730 735
 Glu Thr Leu Lys Ala Leu Lys Gly Ser Val Lys Asp Leu Gly Ile Asn
 740 745 750
 Pro Glu Trp Ile Ser Lys Val Glu Asn Leu Asn Ala Ala Leu Asn Glu
 755 760 765
 Phe Lys Asn Gly Lys Asn Lys Asp Phe Ser Lys Val Thr Gln Ala Lys
 770 775 780
 Ser Asp Leu Glu Asn Ser Ile Lys Asp Val Ile Ile Asn Gln Lys Ile
 785 790 795 800
 Thr Asp Lys Val Asp Asn Leu Asn Gln Ala Val Ser Val Ala Lys Ala
 805 810 815
 Thr Gly Asp Phe Ser Gly Val Glu Gln Ala Leu Ala Asp Leu Lys Asn
 820 825 830
 Phe Ser Lys Glu Gln Leu Ala Gln Gln Ala Gln Lys Asn Glu Asp Phe
 835 840 845
 Asn Thr Gly Lys Asn Ser Ala Leu Tyr Gln Ser Val Lys Asn Gly Val
 850 855 860
 Asn Gly Thr Leu Val Gly Asn Gly Leu Ser Lys Ala Glu Ala Thr Thr
 865 870 875 880
 Leu Ser Lys Asn Phe Ser Asp Ile Lys Lys Glu Leu Asn Ala Lys Leu
 885 890 895
 Gly Asn Phe Asn Asn Asn Asn Asn Asn Gly Leu Glu Asn Ser Thr Glu
 900 905 910
 Pro Ile Tyr Thr Gln Val Ala Lys Lys Val Lys Ala Lys Ile Asp Arg
 915 920 925
 Leu Asp Gln Ile Ala Ser Gly Leu Gly Asp Val Gly Gln Ala Ala Ser
 930 935 940
 Phe Leu Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys Val Gly
 945 950 955 960
 Leu Ser Ala Asn His Glu Pro Ile Tyr Ala Thr Ile Asp Asp Leu Gly
 965 970 975
 Gly Pro Phe Pro Leu Lys Arg His Asp Lys Val Asp Asp Leu Ser Lys
 980 985 990
 Val Gly Leu Ser Arg Glu Gln Lys Leu Thr Gln Lys Ile Asp Asn Leu
 995 1000 1005
 Asn Gln Ala Val Ser Glu Ala Lys Ala Ser His Phe Asp Asn Leu Asp
 1010 1015 1020
 Gln Met Ile Asp Lys Leu Lys Asp Ser Thr Lys Lys Asn Val Val Asn
 1025 1030 1035 1040
 Leu Tyr Val Glu Ser Ala Lys Lys Val Pro Thr Ser Leu Ser Ala Lys
 1045 1050 1055
 Leu Asp Asn Tyr Ala Thr Asn Ser His Thr Arg Ile Asn Ser Asn Val
 1060 1065 1070
 Lys Asn Gly Thr Ile Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys
 1075 1080 1085
 Asn Ser Glu Trp Leu Lys Leu Val Asn Asp Lys Ile Val Ala His Asn
 1090 1095 1100
 Val Gly Ser Ala Pro Leu Ser Ala Tyr Asp Lys Ile Gly Phe Asn Gln
 1105 1110 1115 1120
 Lys Asn Met Lys Asp Tyr Ser Asp Ser Phe Lys Phe Ser Thr Arg Leu
 1125 1130 1135
 Ser Asn Ala Val Lys Asp Ile Lys Ser Gly Phe Val Gln Phe Leu Thr
 1140 1145 1150
 Asn Ile Phe Ser Met Gly Ser Tyr Ser Leu Met Lys Ala Ser Val Glu
 1155 1160 1165
 His Gly Val Lys Asn Thr Asn Thr Lys Gly Gly Phe Gln Lys Ser
 1170 1175 1180

(2) INFORMATION FOR SEQ ID NO:1749:

SUBSTITUTE SHEET (RULE 26)

1286

165 170 175
 Arg Ser Ala Lys Gln Ala Phe Ala Gly Ile Ile Ile Gly Asn Gln Ile
 180 185 190
 Arg Ser Asp Gln Lys Phe Met Gly Val Phe Asp Glu Ser Leu Lys Glu
 195 200 205
 Arg Gln Glu Ala Glu Lys Asn Gly Glu Pro Asn Gly Asp Pro Thr Gly
 210 215 220
 Gly Asp Trp Leu Asp Ile Phe Leu Ser Phe Val Phe Asn Lys Lys Gln
 225 230 235 240
 Ser Ser Asp Leu Lys Glu Thr Leu Asn Gln Glu Pro Val Pro His Val
 245 250 255
 Gln Pro Asp Val Ala Thr Thr Thr Thr Asp Ile Gln Ser Leu Pro Pro
 260 265 270
 Glu Ala Arg Asp Leu Leu Asp Glu Arg Gly Asn Phe Ser Lys Phe Thr
 275 280 285
 Leu Gly Asp Met Asn Met Leu Asp Val Glu Gly Val Ala Asp Ile Asp
 290 295 300
 Pro Asn Tyr Lys Phe Asn Gln Leu Leu Ile His Asn Asn Ala Leu Ser
 305 310 315 320
 Ser Val Leu Met Gly Ser His Asn Gly Ile Glu Pro Glu Lys Val Ser
 325 330 335
 Leu Leu Tyr Gly Asn Asn Gly Gly Pro Glu Ala Arg His Asp Trp Asn
 340 345 350
 Ala Thr Val Gly Tyr Lys Asn Gln Arg Gly Asp Asn Val Ala Thr Leu
 355 360 365
 Ile Asn Val His Met Lys Asn Gly Ser Gly Leu Val Ile Ala Gly Gly
 370 375 380
 Glu Lys Gly Ile Asn Asn Pro Ser Phe Tyr Leu Tyr Lys Glu Asp Gln
 385 390 395 400
 Leu Thr Gly Ser Gln Arg Ala Leu Ser Gln Glu Glu Ile Gln Asn Lys
 405 410 415
 Val Asp Phe Met Glu Phe Leu Ala Gln Asn Asn Ala Lys Leu Asp Asn
 420 425 430
 Leu Ser Lys Lys Glu Lys Glu Lys Phe Gln Asn Glu Ile Glu Asp Phe
 435 440 445
 Gln Lys Asp Ser Lys Ala Tyr Leu Asp Ala Leu Gly Asn Asp His Ile
 450 455 460
 Ala Phe Val Ser Lys Lys Asp Lys Lys His Leu Ala Leu Val Ala Glu
 465 470 475 480
 Phe Gly Asn Gly Glu Leu Ser Tyr Thr Leu Lys Asp Tyr Gly Lys Lys
 485 490 495
 Ala Asp Lys Ala Leu Asp Arg Glu Ala Lys Thr Thr Leu Gln Gly Ser
 500 505 510
 Leu Lys His Asp Gly Val Met Phe Val Asp Tyr Ser Asn Phe Lys Tyr
 515 520 525
 Thr Asn Ala Ser Lys Ser Pro Asp Lys Gly Val Gly Ala Thr Asn Gly
 530 535 540
 Val Ser His Leu Glu Ala Gly Phe Ser Lys Val Ala Val Phe Asn Leu
 545 550 555 560
 Pro Asn Leu Asn Asn Leu Ala Ile Thr Ser Val Val Arg Gln Asp Leu
 565 570 575
 Glu Asp Lys Leu Ile Ala Lys Gly Leu Ser Pro Gln Glu Ala Asn Lys
 580 585 590
 Leu Val Lys Asp Phe Leu Ser Ser Asn Lys Glu Leu Val Gly Lys Ala
 595 600 605
 Leu Asn Phe Asn Lys Ala Val Ala Glu Ala Lys Asn Thr Gly Asn Tyr
 610 615 620
 Asp Glu Val Lys Gln Ala Gln Lys Asp Leu Glu Lys Ser Leu Lys Lys
 625 630 635 640
 Arg Glu Arg Leu Glu Lys Asp Val Ala Lys Asn Leu Glu Ser Lys Ser
 645 650 655
 Gly Asn Lys Asn Lys Met Glu Ala Lys Ser Gln Ala Asn Ser Gln Lys
 660 665 670
 Asp Glu Ile Phe Ala Leu Ile Asn Lys Glu Ala Asn Arg Asp Ala Arg
 675 680 685

SUBSTITUTE SHEET (RULE 26)

1285

Cys Phe Tyr Leu Phe Ala Arg Ile Gln Glu Ala Met Asp Gly Arg Arg
 820 825 830
 Phe Val Leu Asp Ile Asp Glu Ala Trp Lys Tyr Leu Gly Asp Pro Lys
 835 840 845
 Val Ala Tyr Phe Val Arg Asp Met Leu Lys Thr Ala Arg Lys Arg Asn
 850 855 860
 Ala Ile Val Arg Leu Ala Thr Gln Ser Ile Thr Asp Leu Leu Ala Cys
 865 870 875 880
 Pro Ile Ala Asp Thr Ile Arg Glu Gln Cys Pro Thr Lys Ile Phe Leu
 885 890 895
 Arg Asn Asp Gly Gly Asn Leu Ser Asp Tyr Gln Arg Leu Ala Asn Val
 900 905 910
 Thr Glu Lys Glu Phe Glu Ile Ile Thr Lys Gly Leu Asp Arg Lys Ile
 915 920 925
 Leu Tyr Lys Gln Asp Gly Ser Pro Ser Val Ile Ala Ser Phe Asn Leu
 930 935 940
 Arg Gly Ile Pro Lys Glu Tyr Leu Lys Ile Leu Ser Thr Asp Thr Val
 945 950 955 960
 Phe Val Lys Glu Ile Asp Lys Ile Ile Gln Asn His Ser Ile Ile Asp
 965 970 975
 Lys Tyr Gln Ala Leu Arg Gln Met Tyr Gln Gln Ile Lys Glu Tyr
 980 985 990

(2) INFORMATION FOR SEQ ID NO:1748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1183 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...1183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1748

Phe Leu Val Ala Leu Met Ile Pro Asn Leu Asp Ile Glu Gly Glu Thr
 1 5 10 15
 Met Thr Asn Glu Ala Ile Asn Gln Gln Pro Gln Thr Glu Ala Ala Phe
 20 25 30
 Asn Pro Gln Gln Phe Ile Asn Asn Leu Gln Val Ala Phe Ile Lys Val
 35 40 45
 Asp Asn Val Val Ala Ser Phe Asp Pro Asn Gln Lys Pro Ile Val Asp
 50 55 60
 Lys Asn Asp Arg Asp Asn Arg Gln Ala Phe Glu Lys Ile Ser Gln Leu
 65 70 75 80
 Arg Glu Glu Phe Ala Asn Lys Ala Ile Lys Asn Pro Thr Lys Lys Asn
 85 90 95
 Gln Tyr Phe Ser Ser Phe Ile Ser Lys Ser Asn Asp Leu Ile Asp Lys
 100 105 110
 Asp Asn Leu Ile Asp Thr Gly Ser Ser Ile Lys Ser Phe Gln Lys Phe
 115 120 125
 Gly Thr Gln Arg Tyr Gln Ile Phe Met Asn Trp Val Ser His Gln Asn
 130 135 140
 Asp Pro Ser Lys Ile Asn Thr Gln Lys Ile Arg Gly Phe Met Glu Asn
 145 150 155 160
 Ile Ile Gln Pro Pro Ile Ser Asp Asp Lys Glu Lys Ala Glu Phe Leu

SUBSTITUTE SHEET (RULE 26)

1284

290	295	300
Phe Gln Arg Ile Ile Arg Ala Lys Leu Glu Asn Phe Lys Asp Arg Ile		
305	310	315
Glu Leu Ile Glu Glu Leu Leu Ser Lys Tyr His Pro Thr Arg Leu Lys		
	325	330
Glu Tyr Thr Lys Asp Gly Ile Ile Tyr Ser Lys Gln Cys Glu Phe Tyr		
	340	345
Asn Phe Leu Val Gly Met Asn Glu Ala Pro Phe Ile Cys Asn Arg Lys		
	355	360
Asp Leu Tyr Leu Lys Glu Lys Met His Gly Gly Val Lys Glu Val Tyr		
	370	375
Phe Ala Asn Lys His Gly Lys Ile Leu Asn Asp Asp Leu Ser Glu Lys		
	385	390
Tyr Phe Ser Ala Ile Glu Ile Ser Glu Tyr Ala Pro Lys Ser Gln Ser		
	405	410
Asp Leu Phe Asp Lys Ile Asn Ala Leu Asp Ser Glu Phe Ile Phe Met		
	420	425
His Ala Tyr Ser Pro Lys Asn Ser Gln Val Leu Lys Asp Lys Leu Ala		
	435	440
Phe Thr Ser Arg Arg Ile Ile Ser Gly Gly Ser Lys Glu Gln Gly		
	450	455
Met Thr Leu Gly Cys Leu Ser Glu Leu Val Gly Asn Gly Asp Ile Thr		
	465	470
Leu Gly Ser Tyr Gly Asn Ser Leu Val Leu Phe Ala Asp Ser Phe Glu		
	485	490
Lys Met Lys Gln Ser Val Lys Glu Cys Val Ser Ser Leu Asn Ala Lys		
	500	505
Gly Phe Leu Ala Asn Ala Ala Thr Phe Ser Met Glu Asn Tyr Phe Phe		
	515	520
Ala Lys His Cys Ser Phe Ile Thr Leu Pro Phe Ile Phe Asp Val Thr		
	530	535
Ser Asn Asn Phe Ala Asp Phe Ile Ala Met Arg Ala Met Ser Phe Asp		
	545	550
Gly Lys Glu Asp Asn Asn Ala Trp Gly Asn Ser Val Met Thr Leu Lys		
	565	570
Ser Glu Ile Asn Ser Pro Phe Tyr Leu Asn Phe His Met Pro Thr Asp		
	580	585
Phe Gly Ser Ala Ser Ala Gly His Thr Leu Ile Leu Gly Ser Thr Gly		
	595	600
Ser Gly Lys Thr Val Phe Met Ser Met Thr Leu Asn Ala Met Gly Gln		
	610	615
Phe Ala Tyr Asn Phe Pro Ala Asn Ile Ser Lys Asp Lys Gln Lys Leu		
	625	630
Thr Met Val Tyr Met Asp Lys Asp Tyr Gly Ala Tyr Gly Asn Ile Val		
	645	650
Ala Met Gly Gly Glu Tyr Val Lys Ile Glu Leu Gly Thr Asp Thr Gly		
	660	665
Leu Asn Pro Phe Ala Trp Ala Ala Cys Val Gln Lys Thr Asn Ala Thr		
	675	680
Met Glu Gln Lys Gln Thr Ala Ile Ser Val Val Lys Glu Leu Val Lys		
	690	695
Asn Leu Ala Thr Lys Ser Asp Glu Lys Asp Glu Asn Gly Asn Ser Ile		
	705	710
Ser Phe Ser Leu Ala Asp Ser Asn Thr Leu Ala Ala Val Thr Asn		
	725	730
Leu Ile Thr Gly Asp Met Asn Leu Asp Tyr Pro Ile Thr Gln Leu Ile		
	740	745
Asn Ala Phe Gly Lys Asp His Asn Asp Pro Asn Gly Leu Val Ala Arg		
	755	760
Leu Ala Pro Phe Cys Lys Ser Thr Asn Gly Glu Phe Gln Trp Leu Phe		
	770	775
Asp Asn Lys Ala Thr Asp Arg Leu Asp Phe Ser Lys Thr Ile Ile Gly		
	785	790
Val Asp Gly Ser Ser Phe Leu Asp Asn Asn Asp Val Ser Pro Phe Ile		
	805	810
		815

SUBSTITUTE SHEET (RULE 26)

1283

```

Ile Lys Arg Gly Gln Ala Thr Val Phe Ala Tyr Ala Gln Pro Ile Ala
      85          90          95
Met Leu Ala Val Ala Gly Gly Ile Ile Tyr Leu Ser Thr Lys Phe Gly
      100          105          110
Phe Asn Ile Gly Glu Ser Gly Gly Ala Ser
      115          120

```

(2) INFORMATION FOR SEQ ID NO:1747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1747

```

Ser Gly Ile Ser Ile Lys Arg Gly Val Phe Val Ala Ser Lys Gln Ala
1      5      10      15
Asp Glu Gln Lys Lys Leu Val Ile Glu Gln Glu Val Gln Lys Arg Gln
      20      25      30
Phe Gln Lys Ile Glu Glu Leu Lys Ala Asp Met Gln Lys Gly Val Asn
      35      40      45
Pro Phe Phe Lys Val Leu Phe Asp Gly Gly Asn Arg Leu Phe Gly Phe
      50      55      60
Pro Glu Thr Phe Ile Tyr Ser Ser Ile Phe Ile Leu Phe Val Thr Ile
      65      70      75      80
Val Leu Ser Val Ile Leu Phe Gln Ala Tyr Glu Pro Val Leu Ile Val
      85      90      95
Ala Ile Val Ile Val Leu Val Ala Leu Gly Phe Lys Lys Asp Tyr Arg
      100      105      110
Leu Tyr Gln Arg Met Glu Arg Ala Met Lys Phe Lys Lys Pro Phe Leu
      115      120      125
Phe Lys Gly Val Lys Asn Lys Ala Phe Met Ser Ile Phe Ser Met Lys
      130      135      140
Pro Ser Lys Glu Met Ala Asn Asp Ile His Leu Asn Pro Asn Arg Glu
      145      150      155      160
Asp Arg Leu Val Ser Ala Ala Asn Ser Tyr Leu Ala Asn Asn Tyr Glu
      165      170      175
Cys Phe Leu Asp Asp Gly Val Ile Leu Thr Asn Asn Tyr Ser Leu Leu
      180      185      190
Gly Thr Ile Lys Leu Gly Gly Ile Asp Phe Leu Thr Thr Ser Lys Lys
      195      200      205
Asp Leu Ile Glu Leu His Ala Ser Ile Tyr Ser Val Phe Arg Asn Phe
      210      215      220
Val Thr Pro Glu Phe Lys Phe Tyr Phe His Thr Val Lys Lys Lys Ile
      225      230      235      240
Val Ile Asp Glu Thr Asn Arg Asp Tyr Gly Leu Ile Phe Ser Asn Asp
      245      250      255
Phe Met Arg Ala Tyr Asn Glu Lys Gln Lys Arg Glu Ser Phe Tyr Asp
      260      265      270
Ile Ser Phe Tyr Leu Thr Ile Glu Gln Asp Leu Leu Asp Thr Leu Asn
      275      280      285
Glu Pro Val Met Asn Lys Lys His Phe Ala Asp Asn Asn Phe Glu Glu

```

SUBSTITUTE SHEET (RULE 26)

1282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1745

```

Gly Ile Lys Leu Gly Gly Ile Asn Met Ala Gly Thr Gln Ala Ile Tyr
1           5           10           15
Glu Ser Ser Ser Ala Gly Phe Leu Ser Gln Val Ser Ser Ile Ile Ser
          20           25           30
Ser Thr Ser Gly Val Ala Gly Pro Phe Ala Gly Ile Val Ala Gly Ala
          35           40           45
Met Thr Ala Ala Ile Ile Pro Ile Val Val Gly Phe Thr Asn Pro Gln
          50           55           60
Met Thr Ala Ile Met Thr Gln Tyr Asn Gln Ser Ile Ala Glu Ala Val
          65           70           75           80
Ser Val Pro Met Lys Ala Ala Asn Gln Gln Tyr Ser Gln Leu Tyr Gln
          85           90           95
Gly Phe Asn Asp Gln Ser Met Ala Val Gly Thr Ile Ser
          100           105

```

(2) INFORMATION FOR SEQ ID NO:1746:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1746

```

Phe Gln Phe Glu Arg Lys Arg Met Lys Phe Phe Thr Arg Ile Thr Asp
1           5           10           15
Ser Tyr Lys Lys Val Val Val Thr Leu Gly Leu Val Val Thr Thr Asn
          20           25           30
Pro Leu Met Ala Val Thr Ser Pro Ala Thr Gly Val Thr Glu Thr Lys
          35           40           45
Ser Leu Val Ile Gln Ile Ile Ser Val Leu Ala Ile Val Gly Gly Cys
          50           55           60
Ala Leu Gly Val Lys Gly Ile Ala Asp Ile Trp Lys Ile Ser Asp Asp
          65           70           75           80

```

1281

Lys Lys Ser Gln Gln Arg Lys Glu Val Asp Lys Asn Leu His Gln Ile
 260 265 270
 Cys Glu Lys Ile Val Gln Asp Val Lys Ser Arg Ile Glu Ser Tyr Lys
 275 280 285
 Asn Gly Ala Leu Gly Met Ile Glu Glu Leu Asn Ala Gly Phe Asn Lys
 290 295 300
 Leu Val Asp His Tyr Glu Arg Met Lys Arg Gln Leu Glu Glu Ala His
 305 310 315 320
 Glu Lys Leu Gly Tyr Ile Tyr Asn Ser Ile His Leu Thr Ile Ser Asn
 325 330 335
 Arg Arg Ile Gln
 340

(2) INFORMATION FOR SEQ ID NO:1744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1744

Ser Ala Leu Trp His Lys Asp Pro Thr Thr Ile Lys Gln Phe Gly Leu
 1 5 10 15
 Glu Ala Leu Asp Phe Phe Lys Pro His Glu Ile Glu Leu Leu Ile Val
 20 25 30
 Ala Cys Asn Thr Ala Ser Ala Leu Glu Glu Met Gln Lys Tyr
 35 40 45
 Ser Lys Ile Pro Ile Val Gly Val Ile Glu Pro Ser Ile Leu Ala Ile
 50 55 60
 Lys Arg Gln Val Glu Asp Lys Asn Ala Pro Ile Leu Val Leu Gly Thr
 65 70 75 80
 Lys Ala Thr Ile Gln Ser Asn Ala Tyr Asp Asn Ala Leu Lys Gln Gln
 85 90 95
 Gly Tyr Leu Asn Ile Ser His Leu Ala Thr Ser Leu Phe Val Pro Leu
 100 105 110
 Ile Glu Glu Ser Ile Leu Glu Gly Glu Leu Leu Glu Thr Cys Met His
 115 120 125
 Tyr Tyr Phe Thr Pro Leu Glu Ile Leu Pro Glu Val Ile Ile Leu Gly
 130 135 140
 Cys Thr His Phe Pro Leu Ile Ala Gln Lys Ile Glu Gly Tyr Phe Met
 145 150 155 160
 Gly His Phe Ala Leu Pro Thr Pro Pro Leu Leu Ile His Ser Gly Asp
 165 170 175
 Ala Ile Val Glu Tyr Leu Gln Gln Lys Tyr Ala Leu Lys Asn Asn Ala
 180 185 190
 Cys Thr Phe Pro Lys Val Glu Phe His Ala Ser Gly Asp Val Ile Trp
 195 200 205
 Leu Glu Arg Gln Ala Lys Glu Trp Leu Lys Leu
 210 215

(2) INFORMATION FOR SEQ ID NO:1745:

SUBSTITUTE SHEET (RULE 26)

1280

```

      275              280              285
Thr Leu Gly Ala Arg Gly Gly Val Tyr Leu Cys Gly Gly Ile Ile Pro
 290              295              300
Arg Phe Ile Asp Tyr Phe Lys Thr Ser Pro Phe Arg Ala Arg Phe Glu
 305              310              315              320
Thr Lys Gly Arg Met Gly Ala Phe Leu Ala Ser Ile Pro Val His Val
              325              330              335
Val Met Lys Lys Thr Pro Gly Leu Asp Gly Ala Gly Ile Ala Leu Glu
              340              345              350
Asn Tyr Leu Leu His Asp Arg Ile
      355              360

```

(2) INFORMATION FOR SEQ ID NO:1743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...340

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1743

```

Ser Gln Gly Leu Ile Phe Asp Lys Lys Lys Gln Lys Phe Leu Lys Asp
1      5      10      15
Phe Lys Ala Gly Glu Leu Leu Tyr Gln Ser His Phe Lys Pro Leu Val
      20      25      30
Glu Phe Ile Ala Glu Glu Leu Leu Lys Asn Ser Arg Ala Lys Ile Ile
      35      40      45
Gln Ser Asn Cys Asn Lys Ala Leu Lys Val Val Glu Glu Leu Gln Asn
      50      55      60
Thr Ile Lys Thr Thr Ile Glu Lys Gln Ile Asn Pro Gly Met Lys Glu
      65      70      75      80
Thr Gln Asp Pro Gln Gln Glu Ala Arg Phe Asn Leu Asp Arg Ser Thr
      85      90      95
Asp Lys Phe Ile Ser Asp Leu Glu Lys Ser Ala Phe Ser Lys Ile Asn
      100      105      110
Gln Phe Glu Phe Asn Phe Arg Lys Glu Met His Glu Arg Ile Glu Arg
      115      120      125
Gly Ile Gly Asn Asn Glu Cys Lys Glu Ile Phe Gly Asn Glu Leu Lys
      130      135      140
Gln Arg Lys Thr Lys Leu Ile Glu Asp Ile Glu Arg Arg Phe Lys Glu
      145      150      155      160
Cys Glu Glu Gln Phe Arg Gly Ser Val Gly Lys Asn Ile Glu Gln Leu
      165      170      175
Glu Glu Arg Val Lys Asp Ser Leu Ala Ile Ile Lys Arg Ile Asn Asn
      180      185      190
Leu Gly Leu Asn Pro Asn Ser Asn Phe Asn Met Asp Ser Gly Ile Asp
      195      200      205
Thr Ile Gly Leu Phe Ser Ser Ile Gly Gly Leu Val Leu Leu Leu Leu
      210      215      220
Thr Pro Val Val Gly Glu Phe Ala Leu Ile Ala Gly Val Gly Leu Ala
      225      230      235      240
Leu Val Gly Val Gly Lys Ser Ile Trp Ser Phe Phe Asp Ser Asp Tyr
      245      250      255

```

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```

Leu Lys Arg Thr Pro Cys Thr Asn Arg Phe Tyr Leu Lys Ala Leu Leu
   35           40           45
Phe Ala Ile Phe Tyr His Ala Val Asn Asn Phe Leu Thr Gln Cys Pro
   50           55           60
Pro His Gln Val Arg Glu Phe Phe Ser Ser Arg His Ala Gln Gly Trp
   65           70           75           80
Lys Arg Glu Thr Leu Pro Cys Ala Leu Ser Phe Gln Asn Ala Leu
           85           90           95

```

(2) INFORMATION FOR SEQ ID NO:1742:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1742

```

Lys Lys Thr Pro Pro Ile Leu Cys Arg Leu Leu Gly Phe Tyr Ile Leu
1           5           10           15
Lys Lys Leu Pro Gln Arg Cys Phe Met Pro Lys Thr Glu Thr Tyr Pro
   20           25           30
Arg Leu Leu Ala Asp Ile Gly Gly Thr Asn Ala Arg Phe Gly Leu Glu
   35           40           45
Val Ala Pro Arg Gln Ile Glu Cys Val Glu Val Leu Arg Cys Glu Asp
   50           55           60
Phe Glu Ser Leu Ser Asp Ala Val Arg Phe Tyr Leu Ser Lys Cys Lys
   65           70           75           80
Glu Ser Leu Lys Leu His Pro Ile Tyr Gly Ser Phe Ala Val Ala Thr
   85           90           95
Pro Ile Met Gly Asp Phe Val Gln Met Thr Asn Asn His Trp Thr Phe
  100           105           110
Ser Ile Glu Thr Thr Arg Gln Cys Leu Asn Leu Lys Lys Leu Leu Val
  115           120           125
Ile Asn Asp Phe Val Ala Gln Ala Tyr Ala Ile Ser Ala Met Gln Glu
  130           135           140
Asn Asp Leu Ala Gln Ile Gly Gly Ile Lys Cys Glu Ile Asn Ala Pro
  145           150           155           160
Lys Ala Ile Leu Gly Pro Gly Thr Gly Leu Gly Val Ser Thr Leu Ile
  165           170           175
Gln Asn Ser Asp Gly Ser Leu Lys Val Leu Pro Asp Glu Gly Gly His
  180           185           190
Val Ser Phe Ala Pro Phe Asp Asp Leu Glu Ile Leu Val Trp Gln Tyr
  195           200           205
Ala Arg Ser Lys Phe Asn His Val Ser Ala Glu Arg Phe Leu Ser Gly
  210           215           220
Ser Gly Leu Val Leu Ile Tyr Glu Ala Leu Ser Lys Arg Lys Gly Leu
  225           230           235           240
Glu Lys Val Ala Lys Leu Ser Lys Ala Glu Leu Thr Pro Gln Ile Ile
  245           250           255
Ser Glu Arg Ala Leu Asn Gly Asp Tyr Pro Ile Cys Arg Leu Thr Leu
  260           265           270
Asp Thr Phe Cys Ser Met Leu Gly Thr Leu Ala Ala Asp Val Ala Leu

```

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1740

```

Lys Tyr Lys Gly Asp Lys Met Gln Asp Lys Ile Ile Glu Ile Leu Gln
1      5      10      15
Ile Ser Pro Ile Val Pro Val Val Val Glu Asn Ile Lys Asp Ala
      20      25      30
Val Pro Leu Ala Gln Ser Leu Ile Glu Gly Gly Ile Pro Ile Ile Glu
      35      40      45
Val Thr Leu Arg Ser Asn Cys Ala Leu Glu Ala Ile Glu Leu Ile Ala
      50      55      60
Lys Asn Val Pro Lys Met Arg Val Gly Ala Gly Thr Ile Leu Asn Leu
      65      70      75      80
Thr Gln Leu Glu Gln Ala Gln Asn Arg Gly Ala Glu Phe Leu Ile Ser
      85      90      95
Pro Gly Leu Thr Ile Lys Leu Leu Glu His Ala Lys Lys Lys Asp Met
      100      105      110
Pro Leu Ile Pro Gly Val Ser Ser Ser Glu Val Met Gln Ala Leu
      115      120      125
Glu Leu Gly Tyr Asn Ala Leu Lys Phe Phe Pro Ala Glu Tyr Cys Gly
      130      135      140
Gly Val Lys Leu Leu Asn Ala Phe Asn Gly Pro Phe Lys Gly Val Lys
      145      150      155      160
Phe Cys Pro Thr Gly Gly Ile Ser Ala Asp Asn Met Arg Ser Tyr Leu
      165      170      175
Ala Leu Glu Asn Val Val Cys Val Gly Gly Ser Trp Leu Thr Pro Lys
      180      185      190
Asp Leu Ile Gln Asn Lys Glu Trp Asp Lys Ile Thr Glu Ile Cys Lys
      195      200      205
Arg Ala Leu Ala Leu Arg
      210

```

(2) INFORMATION FOR SEQ ID NO:1741:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1741

```

Asn Thr Ala Ile Val Ser Phe Leu Trp Phe Ala Tyr Val Ser Ile Gly
1      5      10      15
Leu Thr Asn Phe Val Ala Val Gly Tyr Met Val Ser Leu Leu Gly Ala
      20      25      30

```

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Glu Asn Tyr Lys Lys Ala Lys Ala Arg Gln Asp Phe Ala Met Gly Lys
 195 200 205
 Ile Asn Arg Glu Glu Leu Leu Lys Val Glu Met Gln Ser Tyr His Asp
 210 215 220
 Val Gly Thr Cys Thr Phe Tyr Gly Thr Ala Asn Ser Asn Gln Met Met
 225 230 235 240
 Met Glu Phe Met Gly Leu His Val Ala Asn Ser Ser Phe Ile Asn Pro
 245 250 255
 Asn Asn Pro Leu Arg Lys Val Leu Val Glu Glu Ser Ala Lys Arg Leu
 260 265 270
 Ala Ser Gly Lys Val Leu Pro Leu Ala Lys Leu Ile Asp Glu Lys Ser
 275 280 285
 Ile Leu Asn Ala Leu Ile Gly Leu Met Ala Thr Gly Gly Ser Thr Asn
 290 295 300
 His Thr Leu His Leu Ile Ala Ile Ala Arg Ser Cys Gly Val Ile Leu
 305 310 315 320
 Asn Trp Asp Asp Phe Asp Ala Ile Ser Asn Leu Ile Pro Leu Leu Ala
 325 330 335
 Lys Val Tyr Pro Asn Gly Ser Ala Asp Val Asn Ala Phe Glu Ala Cys
 340 345 350
 Gly Gly Leu Ala Phe Val Ile Lys Glu Leu Leu Lys Glu Gly Leu Leu
 355 360 365
 Phe Glu Asp Thr His Thr Ile Met Asp Thr Glu Thr Gln Lys Gly Met
 370 375 380
 Gln Asn Tyr Thr Lys Thr Pro Phe Leu Glu Asn Asp Gln Leu Val Tyr
 385 390 395 400
 Lys Asp Ala Val Ser His Ser Leu Asn Thr Asp Ile Leu Arg Pro Val
 405 410 415
 Ser Glu Pro Phe Ala Ala Asn Gly Gly Leu Lys Ile Leu Lys Gly Asn
 420 425 430
 Leu Gly Arg Ala Val Ile Lys Ile Ser Ala Ile Lys Asp Glu His Arg
 435 440 445
 Lys Val Lys Ala Arg Ala Ile Val Phe Lys Thr Gln Ser Glu Phe Leu
 450 455 460
 Glu Arg Phe Lys Asn Lys Glu Leu Glu Arg Asp Phe Val Ala Val Leu
 465 470 475 480
 Pro Phe Gln Gly Pro Lys Ser Asn Gly Met Pro Glu Leu His Lys Leu
 485 490 495
 Thr Thr Asn Leu Gly Ala Leu Gln Asp Met Gly Tyr Lys Val Ala Leu
 500 505 510
 Val Thr Asp Gly Arg Met Ser Gly Ala Ser Gly Lys Val Pro Ser Ala
 515 520 525
 Ile His Leu Ser Pro Glu Gly Ala Leu Asn Gly Ala Ile Ile Lys Ile
 530 535 540
 Lys Asp Gly Asp Leu Ile Glu Leu Asp Ala Pro Asn Asn Ala Leu Asn
 545 550 555 560
 Val Leu Glu Lys Asp Phe Glu Lys Arg Gly Ile Asn Pro Leu Phe Leu
 565 570 575
 Glu Thr Leu Glu Asn Leu Glu Lys Pro Thr Phe Gly Leu Gly Arg Glu
 580 585 590
 Leu Phe Thr Ser Leu Arg Leu Asn Ala Asn Thr Ala Glu Glu Gly Gly
 595 600 605
 Met Ser Phe Gly Ile Lys Val
 610 615

(2) INFORMATION FOR SEQ ID NO:1740:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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```

      195      200      205
Phe Thr Gln Gly Asp Lys Met Arg Lys Val Asp Phe Glu Glu Leu His
 210      215      220
Leu Arg Asn Lys Leu Lys Ser Phe Asn Ser Asn Asp Ala Ala Tyr Leu
225      230      235      240
Gln Gly Thr Asp Tyr Leu Gly Tyr Trp Lys Lys Ala Phe Gly Lys Asn
      245      250      255
Ala Asn Lys Asn Gln Lys Arg Arg Phe Ser Gln Ala Ile Leu Val Ser
      260      265      270
Leu Phe Pro Leu Ala Ser Val Phe Leu Ile Pro Leu Phe Gly Ile Ala
      275      280      285
Asn Pro Arg Phe Lys Thr Asn Trp Ser Tyr Phe His Val Leu Gly Ala
      290      295      300
Val Gly Val Tyr Phe Leu Met Val His Val Ile Ser Thr Asp Leu Phe
305      310      315      320
Leu Met Thr Phe Phe Phe Pro Phe Ile Trp Ala Phe Ile Ser Tyr Leu
      325      330      335
Leu Phe Arg Lys Phe Ile Leu Lys Arg Tyr
      340      345

```

(2) INFORMATION FOR SEQ ID NO:1739:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...615

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1739

```

Ile Leu Ile Glu Gly Val Phe Met Pro Lys His Ser Leu Glu Gln Ile
1      5      10      15
Lys Glu Lys Ile Thr Glu Arg Ser Lys Lys Thr Arg Glu Leu Tyr Leu
      20      25      30
Glu Asn Thr Phe Asn Pro Lys Asn Gln Pro Lys Ile Glu Ser Leu Gly
      35      40      45
Cys Ala Asn Ile Ala His Val Thr Ala Ser Met Pro Glu His Leu Lys
      50      55      60
Met Pro Leu Gly Ser His Lys Arg Lys His Phe Ala Ile Ile Thr Ala
      65      70      75      80
Tyr Asn Asp Met Leu Ser Ala His Gln Pro Phe Lys Asn Tyr Pro Asp
      85      90      95
Leu Ile Lys Lys Glu Leu Gln Glu His Asn Ala Tyr Ala Ser Val Ala
      100      105      110
Ser Gly Val Pro Ala Met Cys Asp Gly Ile Thr Gln Gly Tyr Glu Gly
      115      120      125
Met Glu Leu Ser Leu Phe Ser Arg Asp Val Ile Ala Leu Ser Thr Ala
      130      135      140
Val Gly Leu Ser His Asn Val Phe Asp Gly Ala Phe Phe Leu Gly Val
      145      150      155      160
Cys Asp Lys Ile Val Pro Gly Leu Leu Ile Gly Ala Leu Ser Phe Gly
      165      170      175
Asn Leu Ala Ser Val Phe Val Pro Ser Gly Pro Met Val Ser Gly Ile
      180      185      190

```

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Ala Gln Asn Ala Leu Asn His Ala Asn Thr Arg Leu Ile Leu Glu Lys
 130 135 140
 Pro Leu Gly His Asp Leu Lys Thr Cys Lys Glu Ile Phe Gln Ser Ile
 145 150 155 160
 Ser Ala Phe Phe Lys Glu Glu Gln Ile Phe Arg Ile Asp His Tyr Leu
 165 170 175
 Gly Lys Lys Gly Val Gln Asn Ile Leu Glu Leu Arg Leu Asn Asn Pro
 180 185 190
 Ile Leu Asn Ile Leu Trp Asp Gln Ile Ser Ala Val Glu Ile Cys Val
 195 200 205
 Tyr Glu Thr Leu Gly Val Glu Glu Arg Gly Glu Phe Tyr Asp Lys Ile
 210 215 220
 Gly Ala Leu Arg Asp Met Val Gln Asn His Leu Leu Gln Val Leu Ser
 225 230 235 240
 Leu Ile Ala Thr Asp Leu Pro Asn Asp Leu Lys Asp Leu Arg Gln Glu
 245 250 255
 Lys Ser Lys Phe
 260

(2) INFORMATION FOR SEQ ID NO:1738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1738

Gly Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe
 1 5 10 15
 Ser Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile
 20 25 30
 Ser Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu
 35 40 45
 Val Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Thr Phe Phe Ile Leu
 50 55 60
 Pro Ile Thr Phe Phe Ala Ala Cys Ala Leu Gly Leu Ser Arg Leu Ser
 65 70 75 80
 Tyr Asp His Glu Leu Val Phe Phe Ser Leu Gly Val Ser Pro Lys
 85 90 95
 Lys Met Thr Lys Ala Phe Val Pro Leu Ser Leu Leu Val Ser Ala Ile
 100 105 110
 Leu Leu Ala Phe Ser Leu Ile Leu Ile Pro Thr Ser Lys Ser Ala Tyr
 115 120 125
 Tyr Gly Phe Leu Arg Gln Lys Lys Asp Lys Ile Asp Ile Asn Ile Arg
 130 135 140
 Ala Gly Glu Phe Gly Gln Lys Leu Gly Asp Trp Leu Val Tyr Val Asp
 145 150 155 160
 Lys Thr Glu Asn Asn Ser Tyr Asp Asn Leu Val Leu Phe Ser Asn Lys
 165 170 175
 Ser Leu Ser Gln Glu Ser Phe Ile Leu Ala Gln Lys Gly Asn Ile Asn
 180 185 190
 Asn Gln Asn Gly Val Phe Glu Leu Asn Leu Tyr Asn Gly His Ala Tyr

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```

      210              215              220
Val Ile Val Glu Gly Lys Thr Lys Asp Leu Pro Lys Glu Ile Ala Asn
225              230              235              240
Val Arg Val Ser Gln Asn Leu Thr Arg Gln Ile Glu Leu Ser Trp Asp
      245              250              255
Lys Ser Pro Glu Glu Asp Val Ile Ala Tyr Arg Ile Tyr Ala Ser Asn
      260              265              270
Asn Arg Asn Asp Lys Tyr Lys Phe Ile Ala Gln Thr Thr Asn Thr Ser
      275              280              285
Tyr Val Asp Lys Ile Glu Lys Asp Asn Leu Thr Arg Tyr Tyr Lys Val
      290              295              300
Val Ala Val Asp Lys Thr His Leu Glu Gly Ala Leu Pro Lys Glu Pro
305              310              315              320
Ala Met Gly Glu Thr Ser Asp Arg Pro Glu Ala Pro Ile Ile Thr Lys
      325              330              335
Gly Thr Ile Gln Asp Ser Ser Ala Leu Ile Gln Trp Glu Asn Asn Pro
      340              345              350
Ser Pro Lys Ile Ala Thr Tyr Ala Val Tyr Arg Phe Glu Ala Asn Ser
      355              360              365
Lys Thr Pro Leu Arg Phe Gly Asn Ile Thr Gln Asn Gln Phe Val Asp
      370              375              380
Lys Asp Met Lys Val Gly Val Ala Tyr Arg Tyr Gln Val Val Ser Val
385              390              395              400
Asp Lys Asp Gly Leu Glu Ser His Pro Ser Lys Glu Val Arg Leu Phe
      405              410              415
Leu Glu Arg

```

(2) INFORMATION FOR SEQ ID NO:1737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1737

```

Leu Lys Asn Thr Leu Lys Gly Leu Leu Met Leu Asp Phe Asp Leu Val
1              5              10              15
Leu Phe Gly Ala Thr Gly Asp Leu Ala Met Arg Lys Leu Phe Val Ser
      20              25              30
Leu Tyr Glu Ile Tyr Ile His Tyr Gly Phe Lys Asn Asp Ser Arg Ile
      35              40              45
Ile Ala Ser Gly Arg Lys Glu Leu Ser Asn Glu Glu Phe Leu Ala Leu
      50              55              60
Leu Cys Glu Lys Thr Gln Leu His Ser Arg Glu Lys Gly Glu Glu Phe
      65              70              75              80
Leu Thr His Ile Ser Tyr Leu Arg Val Arg Leu Asp Asn Pro Lys Asp
      85              90              95
Phe Glu Glu Leu Ser Lys Ile Ala Thr Asn Asn Lys Pro Leu Ile Phe
      100              105              110
Tyr Phe Ser Ile Ser Pro Ser Phe Phe Ala Thr Thr Ala Gln Asn Leu
      115              120              125

```

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Ala Pro Ile Gln Ala Gly Met Ile Tyr Lys Met Asn Asp Ala Phe Gly
 195 200 205
 Met Asp Leu Asp Lys Ser Val Gly Ala Ser Leu Val Ala Gly Leu Leu
 210 215 220
 Gly Val Thr Ala Val Ala Gln Val Gly Arg Thr Leu Val Asn Gly Phe
 225 230 235 240
 Leu Lys Phe Ile Pro Val Val Gly Ser Val Ala Gly Gly Ala Thr Ala
 245 250 255
 Ala Val Ile Thr Glu Gly Ile Gly Phe Ala Tyr Leu Lys Val Leu Glu
 260 265 270
 Lys Cys Phe Asn Asp Glu Thr Gly Glu Val Asn Leu Pro Gly Glu Val
 275 280 285
 Gly Met Ile Thr Ser Leu Phe Lys Glu Asn Tyr Leu Asn Leu Asp Thr
 290 295 300
 Ile Lys Lys Leu Lys Pro
 305 310

(2) INFORMATION FOR SEQ ID NO:1736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1736

Met Arg Ser Trp Met Lys Lys Lys Tyr Phe Thr Leu Leu Leu Gln Ser
 1 5 10 15
 Ser Val Val Leu Ala Val Phe Ile Gly Cys Ser Ser Thr Arg Asn His
 20 25 30
 Thr Phe Ser Ala Leu Ser Asn Gln Glu Asn Thr Asp Asp Lys Leu Pro
 35 40 45
 Val Val His Ser Ile Lys Thr Ile Asn Asp Val Ser Ser Val Gly Phe
 50 55 60
 Glu Trp Ser Lys Val Ala Asp Thr Tyr Asp Ile Asp Gly Phe Val Leu
 65 70 75 80
 Tyr Arg Leu Lys Lys Asp Ser Lys Leu Lys Arg Ile Ala Thr Ile Lys
 85 90 95
 Asn Pro Tyr Ala Thr His Tyr Tyr Asp Glu Gly Leu Glu Thr Glu Ser
 100 105 110
 Ser Tyr Thr Tyr Gln Leu Ala Thr Tyr Lys Gly Asp Lys Ile Ser Lys
 115 120 125
 Leu Ser Glu Pro Ile Leu Val Lys Thr Ser Phe Ile Asn Pro Val Glu
 130 135 140
 Ser Val Phe Ala Ser Leu Glu Tyr Pro Lys Ser Val Lys Val Phe Trp
 145 150 155 160
 Ser Pro His Pro Asn Pro Ser Val Ser Lys Tyr Ile Ile Gln Arg Gln
 165 170 175
 Asn Lys Asp Gly Lys Phe Leu Asn Val Gly Ala Val Lys Asn Arg Leu
 180 185 190
 Phe Val Glu Phe Phe Asp Lys Asp Leu Glu Asp Gly Gln Lys Tyr Arg
 195 200 205
 Tyr Gln Ile Ile Ala Glu Asn Phe Met Gly Asp Lys Ser Arg Pro Ser

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```

Asn His Lys Ile Arg Gly Tyr Glu Lys Arg Met Ala Leu Asp Lys Arg
1           5           10           15
Ile Trp Met His Phe Asp Leu Leu Pro Phe Val Phe Ile Ile Pro Leu
          20           25           30
Leu Val Val Ser Phe Leu Leu Ile Phe Glu Ser Ser Ala Val Leu Ser
          35           40           45
Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly Phe Leu Leu Phe Trp Val
          50           55           60
Val Phe Phe Ile Pro Phe Arg Lys Leu Asp Arg Trp Leu Phe Ala Leu
65           70           75           80
Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu Val Asp Phe Met Gly Ser
          85           90           95
Ser Lys Leu Gly Ala Gln Arg Trp Leu Val Ile Pro Phe Thr Ser Ile
          100          105          110
Thr Leu Gln Pro Ser Glu Pro Val Lys Ile Ala Ile Leu Leu Leu Leu
          115          120          125
Ala Arg Phe Asp Gln Asn Gln Pro Thr Ser Phe
          130          135

```

(2) INFORMATION FOR SEQ ID NO:1735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1735

```

Phe Cys Gly Thr Leu Lys Ala Leu Lys Ile Lys Ile Thr Thr Thr Pro
1           5           10           15
Cys Lys Ala Leu Lys Lys Lys Trp Lys Ile Leu Leu Lys His Leu Met
          20           25           30
Lys Lys Lys Pro Leu Met Trp Arg Ile Cys Ala Leu Arg Arg Leu Leu
          35           40           45
Leu Gly Phe Lys Arg Glu Arg Glu Leu Leu Ser Phe Ala Lys His Trp
          50           55           60
Asn Ile Pro Thr Ile Val Val Phe Thr His Thr Gln Ala Glu Ala Gly
65           70           75           80
Asp Ala Phe Val Gln Glu Thr Lys Gly Ile Ile Asp Glu Glu Trp Gly
          85           90           95
Phe Lys Gly Phe Val Arg Ala Tyr Val Arg Val Asn Ser Val Ala Phe
          100          105          110
Ser Phe Arg Gly Leu Lys Val Pro Val Glu Gly Leu Glu Leu Val
          115          120          125
Asp Glu Thr Lys Lys Cys Leu Ser Asp Ala Glu Lys Asn Lys Lys Arg
          130          135          140
His Phe Leu Ser Ile Gln Arg Val Lys Ile Gln Glu Arg Lys Gln Ala
145          150          155          160
Met Ile Glu Glu Cys Lys Thr Ile Ile His Val Ala Ser Gly Ala Ala
          165          170          175
Gly Val Ala Gly Leu Ile Pro Ile Pro Phe Ser Asp Ala Leu Ala Ile
          180          185          190

```

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```

Asn Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn
65                               70       75                               80
Leu Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Leu
                               85                               90       95
Gln Gly Asp Lys Lys Ser Asn Leu Asp Asn Phe Ile Lys Val Val Asp
                               100      105      110
Leu Leu Gln Leu Thr Ile
                               115

```

(2) INFORMATION FOR SEQ ID NO:1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1733

```

Leu His Arg Gln Ala Gln Val Arg Ile Ser Leu Thr Gln Thr Thr Thr
1      5      10      15
Leu Val Ala Thr Ile Gly Ser Asn Ala Pro Tyr Ile Gly Leu Leu Gly
20     25     30
Thr Val Met Gly Ile Met Leu Thr Phe Met Asp Leu Gly Ser Ala Ser
35     40     45
Gly Ile Asp Thr Lys Ala Ile Met Thr Asn Leu Ala Leu Ala Leu Lys
50     55     60
Ala Thr Gly Met Gly Leu Val Ala Ile Pro Ala Ile Val Ile Tyr
65     70     75     80
Asn Leu Leu Val Arg Lys Ser Glu Ile Leu Val Thr Lys Trp Asp Ile
85     90     95
Phe His His Pro Val Asp Thr Gln Ser His Glu Val Tyr Ser Lys Ala
100    105    110

```

(2) INFORMATION FOR SEQ ID NO:1734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1734

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(2) INFORMATION FOR SEQ ID NO:1731:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1731

```

Val Ile Ile Phe Leu Leu Leu Phe Phe Leu Gly Asn Lys Val Phe Ser
1           5           10           15
Ile Tyr Leu Leu Leu Glu Ser Phe Leu Trp Val Ile Leu Thr Thr Trp
          20           25           30
Cys Cys Leu Val Met His Glu Asp Gln Arg Gln Lys Asp Met Glu Gln
          35           40           45
Leu Ile Asn Gly Ile Asp Arg Ile Ile Lys Ala Asn Ser Gly Lys Ser
          50           55           60
Leu His Gln Glu Thr Gln Gln Ala Asn Lys Thr Asp Lys Ala Trp Asp
65           70           75           80
Leu Ala Ala Asn Val Phe Leu Ile Gly Leu Val Val Leu Ala Val Phe
          85           90           95
His Met Ile Lys Arg
          100

```

(2) INFORMATION FOR SEQ ID NO:1732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1732

```

Ala Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile
1           5           10           15
Met Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln
          20           25           30
Thr Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr
          35           40           45
Asp Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser
50           55           60

```

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Gln Asn Leu Ala Leu Arg Lys Ala Phe Glu Asp Leu Cys Ala Glu Phe
 290 295 300
 Asp Cys Glu Leu Val Leu Ala Pro Leu Glu Phe Cys Ser Asp Asn Ala
 305 310 315 320
 Ala Met Ile Gly Arg Ser Ser Leu Glu Ala Tyr Gln Lys Lys Arg Phe
 325 330 335
 Ile Pro Leu Glu Lys Ala Asp Ile Ser Pro Arg Thr Leu Leu Lys Asn
 340 345 350
 Phe Glu

(2) INFORMATION FOR SEQ ID NO:1730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1730

Arg Asn Asn Met Ala Tyr Lys Tyr Asp Arg Asp Leu Glu Phe Leu Lys
 1 5 10 15
 Gln Leu Glu Ser Asp Leu Leu Asp Leu Phe Glu Val Leu Val Phe
 20 25 30
 Gly Lys Asp Gly Glu Lys Arg His Asn Glu Lys Leu Thr Ser Ser Ile
 35 40 45
 Glu Tyr Lys Arg His Gly Asp Tyr Ala Lys Tyr Ala Glu Arg Ile
 50 55 60
 Ala Glu Glu Leu Gln Tyr Tyr Gly Ser Asn Ser Phe Ala Ser Phe Ile
 65 70 75 80
 Lys Gly Glu Gly Val Leu Tyr Lys Glu Ile Leu Cys Asp Val Cys Asp
 85 90 95
 Lys Leu Lys Val Asn Tyr Asn Lys Lys Thr Glu Thr Thr Leu Ile Glu
 100 105 110
 Gln Asn Met Leu Ser Lys Ile Leu Glu Arg Ser Leu Glu Glu Met Asp
 115 120 125
 Asp Glu Glu Val Lys Glu Met Cys Asp Glu Leu Ser Ile Lys Asn Thr
 130 135 140
 Asp Asn Leu Asn Arg Gln Ala Leu Ser Ala Ala Thr Leu Thr Leu Phe
 145 150 155 160
 Lys Met Gly Gly Phe Lys Ser Tyr Gln Leu Ala Val Ile Val Ala Asn
 165 170 175
 Ala Val Ala Lys Thr Ile Leu Gly Arg Gly Leu Ser Leu Ala Gly Asn
 180 185 190
 Gln Val Leu Thr Arg Thr Leu Ser Phe Leu Thr Gly Pro Val Gly Trp
 195 200 205
 Ile Ile Thr Gly Val Trp Thr Ala Ile Asp Ile Ala Gly Pro Ala Tyr
 210 215 220
 Arg Val Thr Ile Pro Ala Cys Ile Val Val Ala Thr Leu Arg Leu Lys
 225 230 235 240
 Thr Gln Gln Ala Asn Glu Asp Lys Lys Ser Leu Gln Ile Glu Ser Val
 245 250 255

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			260					265				270			
Asp	Glu	Ser	Ile	Asn	Val	Ser	Leu	Asn	Ala	Pro	Ile	Leu	Arg	Ala	Ser
		275					280					285			
Thr	Asp	His	Gly	Thr	Ala	Phe	Asp	Ile	Ala	Tyr	Gln	Asn	Lys	Ala	Asn
		290				295					300				
His	Lys	Ser	Tyr	Leu	Asn	Ala	Ile	Lys	Tyr	Leu	Ala				
305					310					315					

(2) INFORMATION FOR SEQ ID NO:1729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1729

Gln	Gly	Ile	Ile	Gln	Ala	Lys	Thr	Pro	Pro	Lys	Asp	Lys	Asp	Met	Ile
1				5					10					15	
Leu	Ser	Ile	Glu	Ser	Ser	Cys	Asp	Asp	Ser	Ser	Leu	Ala	Leu	Thr	Arg
			20					25					30		
Ile	Glu	Asp	Ala	Lys	Leu	Ile	Ala	His	Phe	Lys	Ile	Ser	Gln	Glu	Lys
		35					40					45			
His	His	Ser	Ser	Tyr	Gly	Gly	Val	Val	Pro	Glu	Ile	Ala	Ser	Arg	Leu
	50				55					60					
His	Ala	Glu	Asn	Leu	Pro	Leu	Leu	Leu	Glu	Arg	Val	Lys	Ile	Ser	Leu
65				70					75					80	
Asn	Lys	Asp	Phe	Ser	Lys	Ile	Lys	Ala	Ile	Ala	Ile	Thr	Asn	Gln	Pro
			85						90					95	
Gly	Leu	Ser	Val	Thr	Leu	Ile	Glu	Gly	Leu	Met	Met	Ala	Lys	Ala	Leu
			100				105						110		
Ser	Leu	Ser	Leu	Asn	Leu	Pro	Leu	Ile	Leu	Glu	Asp	His	Leu	Arg	Gly
		115					120					125			
His	Val	Tyr	Ser	Leu	Phe	Ile	Asn	Glu	Lys	Gln	Thr	Arg	Met	Pro	Leu
	130				135						140				
Ser	Val	Leu	Leu	Val	Ser	Gly	Gly	His	Ser	Leu	Ile	Leu	Glu	Ala	Arg
145				150					155					160	
Asp	Tyr	Glu	Asp	Ile	Lys	Ile	Val	Ala	Thr	Ser	Leu	Asp	Asp	Ser	Phe
			165						170					175	
Gly	Glu	Ser	Phe	Asp	Lys	Val	Ser	Lys	Met	Leu	Asp	Leu	Gly	Tyr	Pro
			180					185					190		
Gly	Gly	Pro	Ile	Val	Glu	Lys	Leu	Ala	Leu	Asp	Tyr	Ala	His	Pro	Asn
		195					200					205			
Glu	Pro	Leu	Met	Phe	Pro	Ile	Pro	Leu	Lys	Asn	Ser	Pro	Asn	Leu	Ala
		210				215					220				
Phe	Ser	Phe	Ser	Gly	Leu	Lys	Asn	Ala	Val	Arg	Leu	Glu	Val	Glu	Lys
225				230						235				240	
Asn	Ala	His	Asn	Leu	Asn	Asp	Glu	Val	Lys	Gln	Lys	Ile	Gly	Tyr	His
			245						250					255	
Phe	Gln	Ser	Ala	Ala	Ile	Glu	His	Leu	Ile	Gln	Gln	Thr	Lys	Arg	Tyr
		260						265					270		
Phe	Lys	Ile	Lys	Arg	Pro	Lys	Ile	Phe	Gly	Ile	Val	Gly	Gly	Ala	Ser
		275					280						285		

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```

Phe Ser Ile Thr Asn Ala Ser Gly Asp Ala Ile Val Gly Asn Pro Asp
210                               215                               220
Ser Gln Gly Leu Gly Lys Leu Arg Gln Gly Phe Leu Glu Leu Ser Asn
225                               230                               235                               240
Val Arg Leu Val Glu Glu Met Thr Asp Leu Ile Thr Ala Gln Arg Ala
245                               250                               255
Tyr Glu Ala Asn Ser Lys Ser Ile Gln Thr Ala Asp Ala Met Leu Gln
260                               265                               270
Thr Val Asn Ser Leu Lys Arg
275

```

(2) INFORMATION FOR SEQ ID NO:1728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1728

```

Lys Trp Arg Asn Ser Ser Ser Asp Lys Met Ala Lys Lys Lys Ile Ala
1                               5                               10                               15
Ile Ser Cys Gly Asp Ile Gln Gly Val Gly Leu Glu Leu Ile Leu Lys
20                               25                               30
Ser His Lys Glu Val Ser Ala Leu Cys Glu Pro Leu Tyr Leu Val His
35                               40                               45
Ser Glu Leu Leu Glu Arg Ala Asn Gln Leu Leu Asp Asn Ala Tyr Glu
50                               55                               60
Thr Lys Thr Leu Asn Ala Ile Ala Ile Asp Ala Pro Leu Pro Leu Leu
65                               70                               75                               80
Asn Ser Ser Thr Ile Gly Lys Val Ser Thr Gln Ser Gly Ala Tyr Ser
85                               90                               95
Phe Glu Ser Phe Lys Lys Ala Cys Glu Leu Ala Asp Ser Lys Glu Val
100                              105                              110
Asp Gly Ile Cys Thr Leu Pro Ile Asn Lys Leu Ala Trp Gln Gln Ala
115                              120                              125
Gln Ile Pro Phe Val Gly His Thr Asp Phe Leu Lys Gln Arg Tyr Lys
130                              135                              140
Asp His Gln Ile Ile Met Met Leu Gly Cys Ser Lys Leu Phe Val Gly
145                              150                              155                              160
Leu Phe Ser Asp His Val Pro Leu Ser Ala Val Ser Gln Leu Ile Gln
165                              170                              175
Val Lys Ala Leu Val Lys Phe Leu Leu Ala Phe Gln Lys Ser Thr Gln
180                              185                              190
Ala Lys Ile Val Gln Val Cys Gly Phe Asn Pro His Ala Gly Glu Glu
195                              200                              205
Gly Leu Phe Gly Glu Glu Asp Glu Lys Ile Leu Lys Ala Ile Gln Glu
210                              215                              220
Ser Asn Gln Thr Leu Gly Phe Glu Cys Phe Leu Gly Pro Leu Pro Ala
225                              230                              235                              240
Asp Ser Ala Phe Ala Pro Asn Lys Arg Lys Ile Thr Pro Phe Tyr Val
245                              250                              255
Ser Met Ser His Asp Val Gly Leu Ala Pro Leu Lys Ala Leu Tyr Phe

```

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```

      20      25      30
Val Val Lys Leu Phe Glu Asn Ser Leu Met Glu Val Glu His Gly Lys
      35      40      45
Ile Glu Thr Thr Leu Ser Leu Gly Ala Ser His Leu Glu Val Ile Lys
      50      55      60
Met Met Leu Leu Glu Ser Leu Pro Ser Leu Val Asn Asn Ile Thr Ile
      65      70      75      80
Thr Leu Ile Ser Leu Ile Gly Tyr Ser Ala Met Ala Gly Ala Leu Gly
      85      90      95
Ala Gly Gly Leu Gly Asp Leu Ala Ile Arg Ile Gly Tyr Gln Ser Tyr
      100      105      110
Arg Gly Asp Val Leu Phe Tyr Ala Val Val Val Ile Ile Val Leu Val
      115      120      125
Gln Ile Ile Gln Ser Ala Gly Asp Tyr Val Val Lys Arg Leu Arg Lys
      130      135      140
Asn Lys Tyr
145

```

(2) INFORMATION FOR SEQ ID NO:1727:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1727

```

Ser Tyr Phe Cys Tyr Asn Leu Arg Leu Leu Ser Leu Val Lys Gly Lys
1      5      10      15
Thr Met Leu Arg Ser Leu Tyr Ser Ala Thr Ser Gly Met Leu Ala Gln
      20      25      30
Gln Thr His Ile Asp Thr Thr Ser Asn Asn Ile Ala Asn Val Asn Thr
      35      40      45
Thr Gly Phe Lys Lys Ser Arg Ala Asp Phe Asn Asp Leu Phe Tyr Gln
      50      55      60
Ala Met Gln Tyr Ala Gly Thr Asn Thr Ser Asn Thr Thr Leu Ser Pro
      65      70      75      80
Asp Gly Met Glu Val Gly Leu Gly Val Arg Pro Ser Ala Ile Thr Lys
      85      90      95
Met Phe Ser Gln Gly Ser Pro Lys Glu Thr Glu Asn Asn Leu Asp Ile
      100      105      110
Ala Ile Thr Gly Lys Gly Phe Phe Gln Val Gln Leu Pro Asp Gly Thr
      115      120      125
Thr Ala Tyr Thr Arg Ser Gly Asn Phe Lys Leu Asp Glu Gln Gly Asn
      130      135      140
Leu Val Thr Ser Glu Gly Tyr Leu Leu Ile Pro Gln Ile Thr Leu Pro
      145      150      155      160
Glu Asp Thr Thr Gln Val Asn Ile Gly Val Asp Gly Thr Val Ser Val
      165      170      175
Thr Gln Gly Leu Gln Thr Thr Ser Asn Val Ile Gly Gln Ile Thr Leu
      180      185      190
Ala Asn Phe Val Asn Pro Ala Gly Leu His Ser Met Gly Asp Asn Leu
      195      200      205

```

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(B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1725

```

Val Lys Lys Ser Asn Asn Met Val Val Glu Leu Lys Asn Ile Glu Lys
1      5      10      15
Ile Tyr Glu Asn Gly Phe His Ala Leu Lys Gly Val Asn Leu Glu Leu
      20      25      30
Lys Lys Gly Asp Ile Leu Gly Val Ile Gly Tyr Ser Gly Ala Gly Lys
      35      40      45
Ser Thr Leu Ile Arg Leu Ile Asn Cys Leu Glu Arg Pro Ser Ser Gly
      50      55      60
Glu Val Leu Val Asn Gly Val Asn Leu Leu Asn Leu Lys Pro Lys Glu
      65      70      75      80
Leu Gln Lys Ala Arg Gln Lys Ile Gly Met Ile Phe Gln His Phe Asn
      85      90      95
Leu Leu Ser Ala Lys Asn Val Phe Glu Asn Val Ala Phe Ala Leu Glu
      100     105     110
Ile Ala Arg Trp Glu Lys Thr Lys Ile Lys Ser Arg Val His Glu Leu
      115     120     125
Leu Glu Leu Val Gly Leu Glu Asp Lys Val His Phe Tyr Pro Lys Gln
      130     135     140
Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ser Leu Ala
      145     150     155     160
Asn Cys Pro Asn Leu Leu Cys Asp Glu Ala Thr Ser Ala Leu Asp
      165     170     175
Ser Lys Thr Thr His Ser Ile Leu Thr Leu Leu Ser Gly Ile Gln Lys
      180     185     190
Lys Phe Asp Leu Ser Ile Val Phe Ile Thr His Gln Ile Glu Val Val
      195     200     205
Lys Glu Leu Cys Asn Gln Met Cys Val Ile Ser Ser Gly Glu Ile Val
      210     215     220
Glu Arg Gly Ser Val Glu Glu Ile Phe Ala Asn Pro Lys His Ala Val
      225     230     235     240
Thr Lys Glu Leu Leu Gly Ile Lys Asn Glu His Ala Asp Gln Lys Ser
      245     250     255
Gln Asp Ile Tyr Arg Ile Val Phe Leu Gly Glu His Leu Asp Glu Pro
      260     265     270
Ile Ile Ser Asn Leu Ile Arg Arg Phe Lys Ile Arg Arg
      275     280     285

```

(2) INFORMATION FOR SEQ ID NO:1726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1726

```

Leu Phe Cys Ser Cys Leu Tyr Gln Arg Phe Leu Ile Gly Thr Ser Ile
1      5      10      15
Gly Ser Ser Ala Ser Ile Ile Pro Leu Ala Ile Ser Ala Ile Pro Phe

```

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```

65          70          75          80
Thr Met Pro Asp Asn Leu His Leu His Thr Leu Leu Phe Lys Phe Leu
          85          90          95
Gln Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu
          100          105          110
Ile Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu
          115          120          125
Asp Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Ala Cys Tyr
          130          135          140
Leu Ile Gly Tyr Ala Tyr Leu Asn Arg Gln Val Cys Ala Leu Glu Lys
145          150          155          160
Arg Ala Phe

```

(2) INFORMATION FOR SEQ ID NO:1724:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...90

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1724

```

Met Asn Lys Thr Ile Lys Ala Ala Ala Leu Ala Tyr Asn Met Gly Gln
1          5          10          15
Asp His Ala Pro Lys Val Ile Ala Ser Gly Val Gly Glu Val Ala Lys
          20          25          30
Arg Ile Ile Gln Lys Ala Lys Glu Tyr Asp Ile Ala Leu Phe Ser Asn
          35          40          45
Pro Met Leu Val Asp Ser Leu Leu Lys Val Glu Leu Asp Cys Ala Ile
          50          55          60
Pro Glu Glu Leu Tyr Glu Ser Val Val Gln Val Phe Leu Trp Leu Asn
65          70          75          80
Ser Val Glu Asn Asn Ala Gln Met Ser Lys
          85          90

```

(2) INFORMATION FOR SEQ ID NO:1725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1722

```

Lys Val Leu Trp Val Leu Tyr Phe Leu Thr Ser Leu Phe Ile Cys Ser
1      5      10      15
Leu Ile Val Leu Trp Ser Lys Lys Ser Met Leu Phe Val Asp Asn Ala
20      25      30
Asn Lys Ile Gln Gly Phe His His Ala Arg Thr Pro Arg Ala Gly Gly
35      40      45
Leu Gly Ile Phe Leu Ser Phe Ala Leu Ala Cys Tyr Leu Glu Pro Phe
50      55      60
Glu Met Pro Phe Lys Gly Pro Phe Val Phe Leu Gly Leu Ser Leu Val
65      70      75      80
Phe Leu Ser Gly Phe Leu Glu Asp Ile Asn Leu Ser Leu Ser Pro Lys
85      90      95
Ile Arg Leu Ile Leu Gln Ala Val Gly Val Val Cys Ile Ile Ser Ser
100      105      110
Thr Pro Leu Val Val Ser Asp Phe Ser Pro Leu Phe Ser Leu Pro Tyr
115      120      125
Phe Ile Ala Phe Leu Phe Ala Ile Phe Met Leu Val Gly Ile Ser Asn
130      135      140
Ala Ile Asn Ile Ile Asp Gly Phe Asn Gly Leu Ala Ser Gly Ile Cys
145      150      155      160
Ala Ile Ala Leu Leu Val Ile His Tyr Ile Asp Pro Ser Ser Leu Ser
165      170      175
Cys Leu Leu Ala Tyr Met Val Leu Gly Phe Met Val Leu Asn Phe Pro
180      185      190
Ser Gly Lys Ile Phe
195

```

(2) INFORMATION FOR SEQ ID NO:1723:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1723

```

Gln Phe Val Leu Phe Ala Arg Leu His Gly Ala Trp Val Tyr Gly Val
1      5      10      15
Lys Phe Pro Phe Arg Lys Asp Phe Leu Gly Asp Gly Gly Ala Tyr Phe
20      25      30
Leu Gly Leu Val Cys Gly Ile Ser Leu Leu His Leu Ser Leu Glu Gln
35      40      45
Lys Ile Ser Val Phe Phe Gly Leu Asn Leu Met Leu Tyr Pro Val Ile
50      55      60
Glu Val Leu Phe Ser Ile Leu Arg Arg Lys Ile Lys Arg Gln Lys Ala

```

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1721

```

Met Lys Ser Asp Lys Pro Phe Leu Glu Arg Tyr Phe Tyr Asp Pro Thr
1      5      10      15
Leu Leu Gln Lys Gly Leu Ile Phe Ala Leu Tyr Pro Phe Ser Leu Ile
20      25      30
Tyr Gln Cys Ile Ala Thr Ile Lys Arg Lys Thr Ala Lys Lys His Asp
35      40      45
Phe Lys Ile Pro Ile Ile Ser Ile Gly Asn Leu Ile Ala Gly Gly Ser
50      55      60
Gly Lys Thr Pro Phe Ile Leu Glu Ile Ala Pro Arg Tyr Gln Glu Val
65      70      75      80
Ala Val Val Ser Arg Gly Tyr Gln Arg Asp Ser Lys Gly Leu Val Val
85      90      95
Val Ser Val Lys Gly Asn Ile Leu Val Pro Gln Lys Thr Ala Gly Asp
100     105     110
Glu Ala Tyr Leu Leu Ala Leu Asn Leu Lys Gln Ala Ser Val Ile Val
115     120     125
Ser Glu Lys Arg Glu Leu Gly Val Leu Lys Ala Leu Glu Leu Gly Ser
130     135     140
Lys Ile Val Phe Leu Asp Asp Gly Phe Arg Phe Asn Phe Asn Gln Phe
145     150     155     160
Asn Ala Leu Leu Lys Pro Lys Val Pro Pro Tyr Tyr Pro Phe Cys Leu
165     170     175
Pro Ser Gly Leu Tyr Arg Glu Asn Ile Lys Ser Tyr Lys Glu Ala His
180     185     190
Leu Val Ile Thr Glu Asp Lys Asp Tyr Gln Arg Ile Thr Ser Ile Thr
195     200     205
Asn Pro Thr Lys Arg Met Leu Leu Val Thr Ala Ile Ala Asn Pro Ser
210     215     220
Arg Leu Asp Ala Phe Leu Pro Lys Glu Val Val Lys Lys Leu Tyr Phe
225     230     235     240
Arg Asp His Ala Pro Phe Asp Leu Lys Leu Leu Glu Lys Glu Phe Tyr
245     250     255
Gln Asn Asn Ala Thr Ser Leu Leu Val Thr Ser Lys Asp Leu Val Lys
260     265     270
Leu Gln Asp Cys Lys Leu Pro Leu Ser Val Leu Asp Leu Lys Leu Glu
275     280     285
Ile Cys Pro Lys Val Leu Glu Ile Asp Arg Tyr Ile Leu Ser Tyr
290     295     300
Pro Cys Asn Ile Lys Glu His Leu
305     310

```

(2) INFORMATION FOR SEQ ID NO:1722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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Gly Phe Glu Val Leu Gly Val Lys Glu Leu Val Gln Gln Ser Asp Val
 100 105 110
 Ile Met Ala Leu Leu Pro Asp Glu Leu His Lys Glu Val Leu Glu Lys
 115 120 125
 Glu Val Ile Pro Phe Leu Lys Glu Gly Gln Ile Ile Gly Phe Ala His
 130 135 140
 Gly Phe Ser Val His Phe Asn Gln Val Val Leu Pro Lys Gly Val Gly
 145 150 155 160
 Ala Ile Leu Val Ala Pro Lys Gly Pro Gly Ser Ala Leu Arg Glu Glu
 165 170 175
 Tyr Leu Lys Asn Arg Gly Leu Tyr His Leu Ile Ala Ile Glu Gln Glu
 180 185 190
 Ser Ser Ile His Asn Ala Lys Ala Val Ala Leu Ser Tyr Ala Lys Ala
 195 200 205
 Met Gly Gly Gly Arg Met Gly Val Leu Glu Thr Ser Phe Lys Glu Glu
 210 215 220
 Cys Glu Ser Asp Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Leu
 225 230 235 240
 Glu Ala Ile Val Arg Met Gly Phe Glu Thr Leu Ile Lys Ala Gly Tyr
 245 250 255

(2) INFORMATION FOR SEQ ID NO:1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1720

Gln Thr Ser Arg Ala Thr Thr Leu Glu Val Met Ala Tyr His Met Lys
 1 5 10 15
 Glu Leu Glu Leu Lys Asp Glu Asp Ile Ala Cys Cys Leu Tyr Gly Val
 20 25 30
 Ser Val Phe Leu Gln Glu Lys His Leu Gln Asn Ala Phe Glu Thr Leu
 35 40 45
 Lys Gln Asn Gln Asn Thr Asp Tyr Val Phe Thr Cys Ser Pro Phe Ser
 50 55 60
 Ala Ser Pro Ile Val Leu Leu Ala Leu Lys Thr Ala Phe Lys Trp Leu
 65 70 75 80
 Leu Lys Ser Ile Gln Thr Arg Ala Arg Lys Ile
 85 90

(2) INFORMATION FOR SEQ ID NO:1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...99

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1718

```

Lys Leu Ser Met Arg Ala Ile Ala Ile Val Leu Ala Arg Ser Ser Ser
1          5          10          15
Lys Arg Ile Lys Asn Lys Asn Met Ile Asp Phe Phe Asn Lys Pro Met
          20          25          30
Leu Ala Tyr Pro Ile Glu Thr Ala Leu Asn Ser Lys Leu Phe Glu Lys
          35          40          45
Val Phe Ile Ser Ser Asp Ser Met Glu Tyr Val Asn Leu Ala Lys Asn
          50          55          60
Tyr Gly Ala Ser Phe Leu Asn Leu Arg Pro Lys Asn Leu Ala Asp Glu
          65          70          75          80
Gln Gly His Asp Phe Arg Ser Asp Gly Leu Ser His Glu Arg Ile Arg
          85          90          95
Ile Lys Arg
  
```

(2) INFORMATION FOR SEQ ID NO:1719:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1719

```

Ile Pro Pro Ser Thr Pro Phe Leu Asn Ile Leu His Val Phe Lys His
1          5          10          15
Tyr Arg Ser His Tyr Gly Lys Ile Asn Thr Cys Leu Asn Thr Leu Gly
          20          25          30
Asp Leu Ile Leu Ala Leu Pro Val Tyr Tyr Asp Lys Asp Ile Asp Leu
          35          40          45
Gly Val Ile Gln Ser Leu Gln Val Gly Ile Ile Gly Tyr Gly Val Gln
          50          55          60
Gly Glu Ala Gln Ala Leu Asn Leu Arg Asp Ser Lys Val Lys Val Arg
          65          70          75          80
Ile Gly Leu Tyr Gln Gly Ser Leu Ser Val Ser Lys Ala Lys Lys Glu
          85          90          95
  
```

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```

Ala Leu Lys Leu His Glu Val Leu Ala Asn Asp Leu Lys Thr Ser Gln
 50          55          60
His Phe Asp Val Ser Gln Asn Lys Glu Gln Gly Ala Ile Asn Tyr Ala
 65          70          75          80
Glu Leu Lys Asp Lys Lys Val His Leu Val Ala Leu Val Ser Val Ala
          85          90          95
Val Glu Asn Gly Asn Lys Ile Ser Arg Leu Lys Leu Tyr Asp Val Asp
          100          105          110
Thr Gly Thr Leu Lys Lys Thr Phe Asp Tyr Pro Ile Val Ser Leu Asp
          115          120          125
Leu Tyr Pro Phe Ala Ala His Asn Met Ala Ile Val Val Asn Asp Tyr
          130          135          140
Leu Lys Ala Pro Ser Ile Ala Trp Met Lys Arg Leu Ile Val Phe Ser
          145          150          155          160
Lys Tyr Ile Gly Pro Gly Ile Thr Asn Ile Ala Leu Ala Asp Tyr Thr
          165          170          175
Met Arg Tyr Gln Lys Glu Ile Ile Lys Asn Asn Arg Leu Asn Ile Phe
          180          185          190
Pro Lys Trp Ala Asn Ala Glu Gln Thr Glu Phe Tyr Tyr Thr Gln Met
          195          200          205
Ala Glu Lys Arg Pro Trp Phe
          210          215

```

(2) INFORMATION FOR SEQ ID NO:1717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...114

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1717

```

Phe Leu Arg Gly Lys Phe Ile Gln Glu Arg Leu Lys Ala Leu Cys Cys
 1          5          10          15
Gln Gly Val Glu Gly Glu Phe Gly Val Leu Tyr Gly His Ser Asn Met
          20          25          30
Ile Thr Leu Leu Gln Ala Gly Val Val Glu Ile Glu Thr Glu Asn Gln
          35          40          45
Lys Glu His Ile Ala Ile Asn Trp Gly Tyr Ala Glu Val Thr Asn Glu
          50          55          60
Arg Val Asp Ile Leu Ala Asp Gly Ala Val Phe Ile Lys Lys Gly Ser
          65          70          75          80
Asp Asp Arg Asp Asp Ala Ile Ser Arg Ala Lys Lys Leu Leu Glu Asp
          85          90          95
Ala Ser Ser Asp Arg Leu Ala Val Ser Ser Val Leu Ala Lys Ile Glu
          100          105          110
Ser Leu

```

(2) INFORMATION FOR SEQ ID NO:1718:

(i) SEQUENCE CHARACTERISTICS:

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(2) INFORMATION FOR SEQ ID NO:1715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1715

```

Lys Val Gly Pro Ile Cys Met Ser Lys Ser Ala Ile Phe Val Leu Ser
1          5          10          15
Gly Phe Leu Ala Phe Leu Leu Tyr Ala Leu Leu Leu Tyr Gly Leu Leu
20          25          30
Leu Glu Arg His Asn Lys Glu Ala Glu Lys Ile Leu Leu Asp Leu Asn
35          40          45
Lys Lys Asp Glu Gln Ala Ile Asp Leu Asn Leu Glu Asp Leu Pro Ser
50          55          60
Glu Lys Lys Asn Glu Lys Ile Glu Lys Val Thr Glu Lys Gln Gly Asp
65          70          75          80
Phe Leu Glu Pro Lys Glu Glu Pro Lys Glu Glu Pro Glu Glu Ser Leu
85          90          95
Glu Asp Ile Phe Ser Ser Leu Asn Asp Phe Gln Glu Arg Gln Thr Lys
100         105         110
Thr Leu Lys Lys Thr Ser Lys Lys Met Asn Lys Lys Asn Lys Gly Val
115         120         125

```

(2) INFORMATION FOR SEQ ID NO:1716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1716

```

Gly Arg Thr Met Lys Tyr Leu Trp Leu Phe Leu Ile Tyr Ala Ile Gly
1          5          10          15
Leu Phe Ala Thr Asp Lys Thr Leu Asp Ile Ile Lys Thr Ile Gln Lys
20          25          30
Leu Pro Lys Ile Glu Val Arg Tyr Ser Ile Asp Asn Asp Ala Asn Tyr
35          40          45

```

1257

```

Met Phe Asp Ser Ile Val Tyr Phe Phe Asn Lys Ser Gly Phe Val Thr
      20      25      30
Thr Leu Val Leu Val Trp Ile Ser Leu Tyr Leu Val Met Thr Leu Trp
      35      40      45
Val Phe Leu Tyr Lys Ser Ile Val Leu Lys Ile Glu Leu Arg Arg Glu
      50      55      60
Met Gln Ser Leu Ser Asn Ile Leu Asn Gly Ala Gln Asp Ala Gln Ser
      65      70      75      80
Ile Leu Cys Leu Ile Lys Lys Glu Met Met Arg Pro Lys Gly Ile Leu
      85      90      95
Met Asn Cys Cys Arg Ala Trp Lys His Gln Val Leu Lys Gln Ser Thr
      100      105      110
Thr Gly Leu Val Val Leu Ser Ile Ile Ser Ser Thr Ala Pro Phe Ile
      115      120      125
Gly Leu Phe Gly Thr Val Val Glu Ile Leu Glu Ala Phe Asn Asn Leu
      130      135      140
Gly Ala Leu Gly Gln Ala Ser Phe Gly Val Ile Ala Pro Ile Ile Ser
      145      150      155      160
Lys Ala Leu Ile Ala Thr Ala Ala Gly Ile Leu Ala Ala Ile Pro Ala
      165      170      175
Tyr Ser Phe Tyr Leu Ile Leu Lys Arg Lys Val Tyr Asp Leu Ser Val
      180      185      190
Tyr Val Gln Met Gln Val Asp Ile Leu Ser Ser Lys Lys
      195      200      205

```

(2) INFORMATION FOR SEQ ID NO:1714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1714

```

Lys Val Phe Met Asn Tyr Asp Asn Tyr Trp Asp Glu Asp Lys Pro Glu
1      5      10      15
Leu Asn Ile Thr Pro Leu Val Asp Val Met Leu Val Leu Leu Ala Ile
      20      25      30
Leu Met Val Thr Thr Pro Thr Leu Thr Tyr Lys Glu Glu Ile Ala Leu
      35      40      45
Pro Ser Gly Ser Lys Thr Ala Arg Ala Thr Gln Asp Lys Val Ile Glu
      50      55      60
Ile Arg Met Asp Lys Asp Ala Lys Ile Tyr Ile Asp Ser Gln Thr Tyr
      65      70      75      80
Glu Tyr Asn Ser Phe Pro Asp Thr Phe Asn Leu Leu Ser Lys Lys Tyr
      85      90      95
Asp Lys Asp Thr Arg Val Ser Ile Arg Ala Asp Lys Arg Leu Thr Tyr
      100      105      110
Asp Lys Val Ile Tyr Leu Leu Lys Thr Ile Lys Glu Ala Gly Phe Leu
      115      120      125
Lys Val Ser Leu Ile Thr Ser Pro
      130      135

```

1256

305
Gln

310

315

320

(2) INFORMATION FOR SEQ ID NO:1712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1712

```

Arg Ser Gly Asn Thr Thr Leu Pro Tyr Lys Arg Ser Ser Ser Leu Thr
1          5          10          15
Ala Arg Ala Leu Val Leu Ser Ser Asp Pro Val Glu Phe Lys Glu Ala
          20          25          30
Ser Gly Lys Tyr Trp Leu Ser Val Asn Gln Asn Ala Tyr Leu Lys Ile
          35          40          45
Ser Ser Asn Asn Pro Leu Trp Gln Pro Lys Ile Ile Phe Tyr Asp Glu
          50          55          60
Asn Leu Lys Ile Ile Gln Ile Ile Ala Lys Glu Asn Arg Gln Gln Glu
65          70          75          80
Ile Ala Leu Asn Leu Leu Asp Gly Val Arg Phe Ile His Ile Thr Asp
          85          90          95
Ala Lys Asn Pro Ile Ile Leu Lys Asn Gly Ile Ser Val Val Phe Asp
          100          105          110
Ala Met Pro
          115

```

(2) INFORMATION FOR SEQ ID NO:1713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...205

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1713

```

Arg Ser Leu Ala Cys Trp Leu Arg Leu Ser Leu Phe Lys Gly Ile Ile
1          5          10          15

```

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Ile Arg Arg Val Ser Leu Lys Glu Trp Glu Tyr Asp Phe Ala Leu Gln
 165 170 175
 Lys Ile Lys Leu Pro Asn Gly Glu Ser Leu Ser Phe Glu
 180 185

(2) INFORMATION FOR SEQ ID NO:1711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1711

Met Glu Gln Asn Lys Lys Ser Leu Glu Asn Leu Asp Leu Ser Asp Val
 1 5 10 15
 Gln Asn Ile Ser Lys Asp Ile Ser Gly Thr Ala Leu Glu Glu Leu Ser
 20 25 30
 Leu Lys Asn Leu Asp Lys Asn Leu Gln Ile Leu Lys Glu Val Gly Ala
 35 40 45
 Ala Glu Ile Cys Lys Ala Thr Lys Ile Ala Ser Lys Asn Ile His Ser
 50 55 60
 Ile Leu Glu Lys Arg Tyr Glu Ser Leu Ser Arg Val His Ala Arg Gly
 65 70 75 80
 Phe Ile Gln Ile Leu Glu His Glu Tyr Lys Ile Asp Leu Ser Ala Trp
 85 90 95
 Val Lys Glu Phe Asp Lys Val Cys Val Phe Lys Glu Gly Val Gly Glu
 100 105 110
 Glu Gln Lys Gln Glu Thr Ser Pro Glu Glu Thr Ala Lys Lys Pro Leu
 115 120 125
 Lys Val Glu Leu Asp Tyr Ser Ile Asn Gln Ala Asn Thr Ser Leu Ser
 130 135 140
 Lys Lys Ser Ser Lys Trp Lys Pro Phe Val Ile Val Leu Gly Val Val
 145 150 155 160
 Val Ile Ile Leu Val Val Ile Ile Gln Asn Ser Ser Ser Leu Lys
 165 170 175
 Glu Glu Arg Glu Gln Glu Arg Ala Ile Lys Pro Asp Thr Lys Asn Asn
 180 185 190
 Ser Phe Asn Glu Thr Asn Pro Thr Glu Glu Lys Lys Leu Glu Pro Thr
 195 200 205
 Pro Lys Leu Glu Glu Lys His Lys Glu Gln Asp Lys Gln Gly Lys Glu
 210 215 220
 Ala Ile Lys Glu Asn Pro Asn Thr Ile Tyr Ile Ile Pro Lys Arg Asp
 225 230 235 240
 Ile Trp Val Glu Val Ile Asp Leu Asp Glu Lys Lys Asn Ser Phe Gln
 245 250 255
 Lys Val Phe Lys Lys Ser Tyr Pro Leu Glu Ala Lys Asn His Arg Leu
 260 265 270
 Leu Leu Arg Phe Gly His Gly His Leu Ile Leu Lys Asn Asn His Gln
 275 280 285
 Glu Gln Asp Tyr Asn Asp Ser Lys Thr Arg Arg Phe Leu Tyr Glu Pro
 290 295 300
 Asn Lys Gly Leu Thr Leu Ile Asn Glu Ala Gln Tyr Lys Ala Leu Gln

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1709

```

Thr Pro Met Gly Thr Ser Thr His Tyr Asn Asp Trp Tyr Glu Ser Ile
1          5          10          15
Ala Leu Lys Asn Val Phe Gly Ser Lys Glu Lys Val Pro Pro Val Ser
          20          25          30
Ser Thr Lys Gly Gln Ile Gly His Cys Leu Gly Ala Ala Gly Ala Leu
          35          40          45
Val Ala Val Ile Ser Ile Met Ala Met Asn Gln Gly Ile Leu Pro Pro
          50          55          60
Thr Ile Asn Gln Glu Thr Pro Asp Pro Glu Cys Asp Leu Asp Tyr Ile
65          70          75          80
Pro Asn Thr Ala Arg Glu Lys Gln Val Asn Ala Val Met Ser Asn Ser
          85          90          95
Phe Gly Phe Gly Gly Thr Asn Gly Val Val Ile Phe Lys Lys Ala
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:1710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1710

```

Gly Pro Ile Gln Ser Ala Pro Ala Met Asn Lys Leu Phe Leu Ala Phe
1          5          10          15
Ile Val Gly Gly Met Leu Leu Ser Ala Asp Ala Leu Asn Asp Lys Ile
          20          25          30
Glu Asn Leu Met Gly Glu Arg Ser Tyr His Met Asn Lys Leu Phe Leu
          35          40          45
Glu Arg Leu Phe Lys Asn Arg Lys Asp Phe Tyr Glu Met Gly Arg Leu
          50          55          60
Asp Ser Leu Lys Leu Leu Asn Thr Leu Lys Glu Asn Gly Leu Leu Ser
65          70          75          80
Phe Asn Phe Asp Lys Pro Ser Val Leu Lys Ile Thr Phe Lys Ala Ser
          85          90          95
Ser Asn Pro Leu Ala Phe Ala Lys Ser Ile Asn Asn Ser Leu Asn Met
          100          105          110
Met Gly Tyr Ser Tyr Val Leu Pro Ile Arg Met Gln Ser Ser Ser Gly
          115          120          125
Glu Asn Val Phe Ser Tyr Glu Leu Lys Thr Glu Tyr Val Leu Asp Pro
          130          135          140
Asn Ile Leu Ile Glu Thr Met Lys Arg His Gly Phe Asp Phe Met Asp
145          150          155          160

```

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```

Trp Tyr Phe Lys Lys Glu Arg Asn Pro Met Val Ile His Glu Lys Ile
1      5      10      15
Lys Ser Arg Phe Ser Arg Asn Trp Ser Leu Arg Asn Arg Gly Arg His
      20      25      30
Phe Ala Ser Ser Ser Val Tyr Phe Ser Leu Leu Val Ile Thr Ala
      35      40      45
Val Asn Arg Ser Ser Ala Val Ala Trp Leu Leu Met Pro Glu His Leu
      50      55      60
Ile Gly Trp Phe Leu Ile Ser Phe Ser Gly Glu Phe Val Ala Asp Met
65      70      75      80
Ala Phe Gly Lys Lys Ser Lys Ile Phe Lys Thr Arg Phe Gly Ile Ser
      85      90      95
Ile Val Ser Gly Val Ser Leu Leu Leu Gly Ala Leu Pro Ala His Leu
      100      105      110
Phe Phe Val Trp Phe Gly Phe Ile Asn Trp Trp Ala Val Phe Phe Ile
      115      120      125
Glu Ala Gly Ala Asp Leu Leu Val Gly Cys Val Ile Gln Lys Ile Phe
130      135      140
Phe Gly Lys Tyr Trp Val Asp Arg Tyr Tyr
145      150

```

(2) INFORMATION FOR SEQ ID NO:1708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1708

```

Trp Ala Lys Gly Ala Gly Ala Leu Val Leu Glu Glu Tyr Glu Ser Ala
1      5      10      15
Lys Lys Arg Gly Ala Lys Ile Tyr Ala Glu Phe Ala Gly Tyr Gly Glu
      20      25      30
Ser Gly Asp Ala Asn His Ile Thr Ala Pro Ala Pro Glu Gly Glu Arg
      35      40      45
Ala Phe Lys Ala Met Lys Met Ala Leu Glu Met Ala Lys Val Glu Val
      50      55      60
Cys Tyr Val Asn Ala His Gly Asp Lys His Ala Leu
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:1709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1706

```

Cys Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu
1           5           10           15
Ile Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp
20           25           30
Arg Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn
35           40           45
Val Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys
50           55           60
Glu Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Asp Leu Lys
65           70           75           80
Glu Arg Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr
85           90           95
Thr Pro Thr Phe Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser
100          105          110
Val Ser Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly
115          120          125
Leu Val Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly
130          135          140
Arg Leu Asn Gly Phe Leu Asn Ala His Lys Arg Cys Ala Tyr Ser Val
145          150          155          160
Met Ile Gly Gln Asn Gln Val Leu Gly Phe Ile Gly Thr Asn Phe Lys
165          170          175
Gln Glu Leu Val Val Asp Phe Ile Val Pro Ser Ala Glu Ile Asn Ile
180          185          190
Gly Asp Gln Val Leu Thr Ser Gly Leu Asp Gly Ile Phe Gly Ala Gly
195          200          205
Val Phe Val Gly Glu Val Ser Ser Val Glu Asp His Tyr Thr Tyr Lys
210          215          220
Ser Ala Val Leu Lys Asn Ala Phe Leu Ser Glu Ala Lys Leu Leu Arg
225          230          235          240
His Val Phe Leu Ser Gly Val Lys Asn
245

```

(2) INFORMATION FOR SEQ ID NO:1707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1707

1251

```

Thr Arg Pro Ser Val Ile Leu Phe Leu Asn Ile Gly Leu Asp Asp Asp
530          535          540
Ala Lys Lys Leu Val Lys Gln Ser Phe Gly Arg Gly Val Arg Ile Glu
545          550          555          560
Ser Val Lys Asn Gln Arg Gln Arg Leu Ala Tyr Leu Glu Ile Asp Glu
          565          570          575
Ala Ile Lys Asp Lys Leu Lys Pro Asn Ala Ala Met Leu Glu Met Leu
          580          585          590
Phe Val Ile Pro Thr Asn His Ala Ser Leu Glu Ala Ile Leu Lys Phe
          595          600          605
Gln Lys Glu Ser Glu Asn Gly Gly Glu Asn Arg Gly Pro Trp Arg Glu
610          615          620
Ile Lys Leu Glu Lys Thr Arg Ile Glu His Ala Leu Phe Val Pro Cys
625          630          635          640
Tyr Arg Lys Glu Gln Thr Asn Ala Leu Lys Ile Ser Gln Ser Ala Ser
          645          650          655
Phe Lys Met Ser Glu Lys Asn Phe Lys Asp Leu Lys Glu His Phe His
          660          665          670
Leu Met Ser Glu Lys His Phe Ile Leu Lys His Glu Ile Tyr Asp Pro
675          680          685
Lys Asp Tyr Ala Leu Leu Lys Glu Met Ile Gln Thr Ala His Phe Lys
690          695          700
Lys Val Ser Thr Trp His Tyr Lys Asp Leu Asp Tyr Met Ile Ser Glu
705          710          715          720
Ile Lys Gly Lys Leu Tyr Pro Asn Gln Lys Val Pro Lys Asp Glu Phe
          725          730          735
Asn Ala Leu Asp Asn Glu Lys Ile Val His Phe Lys Arg Val Lys Val
          740          745          750
Lys Ala Asp Lys Lys Glu Lys Leu Ile Gln Thr Ile Gln Glu Val Lys
          755          760          765
Glu His Ala Pro Leu Asp Lys Glu Thr Leu Arg Lys Lys Ile Ala Gln
770          775          780
Gly Glu Ile Asp Pro Tyr Asp Thr Glu Lys His Lys Gln Asp Arg Thr
785          790          795          800
Phe Lys Val Gly Asp Ala Glu Leu Leu Lys Leu Lys Glu His Tyr Tyr
          805          810          815
Thr Pro Leu Ile Lys Ala Lys Asn Cys Asp Trp Leu Lys His Val Val
          820          825          830
Lys Val Lys Ser Glu Ser Asp Phe Leu Glu Glu Leu Lys Ile Thr
835          840          845
Glu Thr Leu Gln Glu Asn Tyr Asp Phe Trp Ala Phe Ser Lys Ile Asp
850          855          860
Glu His Leu Asp Asn Leu Phe Ile Pro Tyr Ile Asp Asn Ala Thr Glu
865          870          875          880
Arg Arg Phe Phe Pro Asp Phe Ile Phe Trp Leu Gln Lys Gly Gly Thr
          885          890          895
Gln Ile Ile Cys Phe Ile Asp Pro Lys Gly Ser Lys His Thr Asp Tyr
          900          905          910
Glu His Lys Ala Asp Ala Tyr Gln Leu Phe Glu Asp Lys Val Phe Asn
915          920          925
Pro Lys Asp Asp Pro Asn Leu Lys Ile Lys Val Val Leu Lys Phe Tyr
930          935          940
Gly Asp Lys Asp Asp Val Gly Glu Arg Tyr Arg Asp Leu
945          950          955

```

(2) INFORMATION FOR SEQ ID NO:1706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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1	5	10	15
Phe Val Ala Gln Lys Leu Ala Glu Glu Glu Leu Asn Ala Asn Glu Ile			
20	25	30	
Asn Asp Pro Leu Glu Met Leu Asp Phe Lys Ser Phe Asp Asp Asn Lys			
35	40	45	
Glu Leu Leu Asp Tyr Gln Gln Ala Leu Ile Asn Ala Phe Arg Val			
50	55	60	
Leu Val Ala Tyr Phe Arg Asp Phe Lys Glu Ser Lys Lys Glu Phe Tyr			
65	70	75	80
Ala Phe Tyr Gln Lys His Tyr Ser Phe Ala Asn Cys Asp Phe Ala Lys			
85	90	95	
Lys Lys Leu Asn His Leu Leu Lys Ser His Phe Lys Val Glu Asn His			
100	105	110	
Cys Val Arg Phe Glu Asn Phe Ile Asn Arg Leu Ala Phe Tyr Met Ala			
115	120	125	
Thr Gly Ser Gly Lys Thr Ile Val Ile Ile Lys Leu Val Glu Leu Leu			
130	135	140	
Ser Val Ala Met Gly Met Gly Leu Ile Pro Lys Lys Asn Ile Met Phe			
145	150	155	160
Phe Ser Ala Asn Glu His Leu Ile Lys Gln Phe Glu Lys Glu Ile Glu			
165	170	175	
Lys Tyr Asn Arg Asn Lys Asp Tyr Ser Lys Gln Ile Asp Phe Lys Asn			
180	185	190	
Leu Lys Ser Val Lys Asn Lys Asp Phe Tyr Arg Ala Pro Lys Asp Ser			
195	200	205	
Leu Met Lys Glu Ile Ala Leu Phe Tyr Tyr Arg Ala Asp Leu Met Ser			
210	215	220	
Asp Glu Glu Ser Lys Glu Asn Leu Leu Asn Tyr Lys Asp Cys Trp Asp			
225	230	235	240
Asn Gly Glu Asn Tyr Val Ile Leu Asp Glu Ala His Lys Gly Asn Lys			
245	250	255	
Thr Glu Ser Lys Arg Gln Ala Ile Phe Ser Leu Leu Ser Leu Lys Gly			
260	265	270	
Phe Leu Phe Asn Phe Ser Ala Thr Phe Thr Glu Glu Ser Asp Leu Ile			
275	280	285	
Thr Ala Val Tyr Asn Leu Ser Val Gly Glu Trp Val Lys Leu Gly Tyr			
290	295	300	
Gly Lys Glu Ser Val Leu Leu Lys Lys Asn Asn Leu Asn Ala Phe Lys			
305	310	315	320
Glu Leu Lys Asp Leu Asn Asp Arg Glu Lys Glu Ile Ala Leu Leu Lys			
325	330	335	
Ala Leu Leu Leu Leu Gly Met Gln Lys Arg Tyr Lys Val Glu Gly Tyr			
340	345	350	
Phe His Asp Pro Leu Met Leu Val Phe Thr His Ser Val Asn Met Glu			
355	360	365	
Asn Ser Asp Ala Glu Ile Phe Phe Lys Thr Leu Ala Arg Val Ile Glu			
370	375	380	
Asn Asp Asp Glu Ser Asp Phe Ser Lys Ala Lys Asp Asp Leu Leu Glu			
385	390	395	400
Glu Leu Lys Asn Pro Glu Phe Leu Phe Ser Asp Gly Lys Asp Lys Glu			
405	410	415	
Lys Asp Tyr Lys Ile Glu Val Phe Lys Glu Ser Leu Lys Gly Met Asp			
420	425	430	
Phe Lys Gly Leu Lys Glu Ala Val Phe Tyr Ala Ser Asn Gly His Ile			
435	440	445	
Glu Val Ile Ile Asn Pro Lys Asn Asn Gln Glu Ile Ala Phe Lys Leu			
450	455	460	
Asn Thr Ser Asp Lys Val Phe Cys Leu Ile Arg Ile Gly Asp Ile Thr			
465	470	475	480
Glu Trp Ile Arg Glu Lys Leu Lys Ser Val Lys Val Val Ser Lys Asn			
485	490	495	
Leu Ser Phe Lys Glu Glu Ser Tyr Phe Ser Gln Ile Asp Lys Ser Ser			
500	505	510	
Ile Asn Ile Leu Val Gly Ser Arg Ala Phe Asp Thr Gly Trp Asp Ser			
515	520	525	

1249

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1704

```

Lys Gly Thr Ser Met Ser Glu Gln Arg Lys Glu Ser Leu Gln Asn Asn
1      5      10      15
Pro Asn Leu Ser Lys Lys Asp Ile Lys Ile Val Glu Lys Ile Leu Ser
      20      25      30
Lys Asn Asp Ile Lys Ala Ala Glu Met Lys Glu Arg Tyr Leu Lys Glu
      35      40      45
Gly Ser Val Cys Val Asn Phe Met Ser Ser Pro Gly Ser Gly Lys Thr
      50      55      60
Thr Met Leu Glu Asn Leu Ala Asp Phe Lys Asp Phe Lys Phe Cys Val
      65      70      75      80
Val Glu Gly Asp Leu Gln Thr Asn Arg Asp Ala Asp Arg Leu Arg Lys
      85      90      95
Lys Gly Val Ser Ala His Gln Ile Thr Thr Gly Glu Ala Cys His Leu
      100     105     110
Glu Ala Ser Met Ile Glu Gly Ala Phe Asp Leu Leu Lys Asp Glu Gly
      115     120     125
Ala Leu Glu Lys Ser Asp Phe Leu Ile Ile Glu Asn Val Gly Asn Leu
      130     135     140
Val Cys Pro Ser Ser Tyr Asn Leu Gly Ala Ala Met Asn Ile Val Leu
      145     150     155     160
Leu Ser Val Pro Glu Gly Asp Asp Lys Val Leu Lys Tyr Pro Thr Met
      165     170     175
Phe Met Cys Ala Asp Ala Val Ile Ile Ser Lys Ala Asp Met Ile Glu
      180     185     190
Val Phe Asn Phe Arg Val Ser Gln Val Lys Glu Asp Met Gln Lys Leu
      195     200     205
Lys Pro Glu Ala Pro Ile Phe Leu Met Ser Ser Lys Asp Pro Lys Ser
      210     215     220
Leu Glu Asp Phe Lys Asn Phe Leu Leu Glu Lys Lys Arg Glu Asn Tyr
      225     230     235     240
Gln Ser Thr His Ser Phe
      245

```

(2) INFORMATION FOR SEQ ID NO:1705:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 957 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...957

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1705

Glu Lys Ile Met Ala Lys Lys Lys Gln Glu Val Arg Asn Asn Glu Ile

1248

```

      35              40              45
Asn Ser Leu Ile Phe Gly Ser Leu Ile His Asn Ala Lys Glu Ile Asn
  50              55              60
Arg Leu Glu Lys Asn Phe Asn Val Lys Ile Glu Glu Asp Pro Lys Lys
  65              70              75              80
Ile Pro Lys Asn Lys Ser Val Ile Ile Arg Thr His Gly Ile Pro Lys
      85              90              95
Gln Asp Leu Glu Tyr Leu Lys Asn Lys Gly Val Lys Ile Thr Asp Ala
      100              105              110
Thr Cys Pro Tyr Val Ile Lys Pro Gln Gln Ile Val Glu Ser Met Ser
      115              120              125
Lys Glu Gly Tyr Gln Ile Val Leu Phe Gly Asp Ile Asn His Pro Glu
      130              135              140
Val Lys Gly Val Ile Ser Tyr Ala Thr Asn Gln Ala Leu Val Val Asn
      145              150              155              160
Ser Leu Glu Glu Leu Gln Glu Lys Lys Leu Gln Arg Lys Val Ala Leu
      165              170              175
Val Ser Gln Thr Thr Lys Gln Thr Pro Lys Leu Leu Gln Ile Ala Ser
      180              185              190

```

(2) INFORMATION FOR SEQ ID NO:1703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1703

```

Lys Leu Pro Ile His Ala Phe Val Leu Met Cys Leu Ala Ile Pro Ser
  1              5              10              15
Lys Val Ile Ala Ile Asn Asp Asn Val Ala Leu Leu Glu Thr Leu Gly
      20              25              30
Val Gln Arg Glu Ala Ser Leu Asp Leu Met Gly Glu Ser Val Lys Val
      35              40              45
Gly Asp Tyr Val Leu Leu His Ile Gly Tyr Val Met Ser Lys Ile Asp
      50              55              60
Glu Lys Glu Ala Leu Glu Ser Ile Glu Leu Tyr Gln Glu Met Ile Ala
      65              70              75              80
Glu Val Asn Glu Thr His Glu
      85

```

(2) INFORMATION FOR SEQ ID NO:1704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

1247

```

Gly Arg Glu Asp Asn His Phe Ala Pro Leu Ala Ile Val Gly Gly Pro
130          135          140
Leu Lys Ala Cys Asp Tyr Glu Ser Pro Ile Ala Ser Ala Gln Val Lys
145          150          155          160
Ser Ala Phe Ile Leu Ser Ala Leu Gln Ala Gln Gly Ile Ser Ala Tyr
          165          170          175
Lys Glu Ser Glu Leu Ser Arg Asn His Thr Glu Ile Met Leu Lys Ser
          180          185          190
Leu Gly Ala Asn Ile Gln Asn Gln Asp Gly Val Leu Lys Ile Ser Pro
          195          200          205
Leu Glu Lys Pro Leu Glu Ser Phe Asp Phe Thr Ile Ala Asn Asp Pro
210          215          220
Ser Ser Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr Pro Lys Ser
225          230          235          240
Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg Ile Glu Ala
          245          250          255
Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr Val Ile Gln
          260          265          270
Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu His Ala Pro
275          280          285
Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu Ile Asp Glu
290          295          300
Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly Lys Ser Met
305          310          315          320
Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp Arg Ile Lys
          325          330          335
Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys Glu Glu Phe
          340          345          350
Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser Gln Leu Lys
          355          360          365
Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser Phe Asn Asp
370          375          380
His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala Leu Pro Leu
385          390          395          400
Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro Thr Phe Gln
          405          410          415
Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly Asn
          420          425          430

```

(2) INFORMATION FOR SEQ ID NO:1702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1702

```

Asn Ala Arg Thr Phe Leu Ser Gln Pro Phe Ser Phe Gly Ser Ile Tyr
1          5          10          15
Ser Lys Lys Gly Val Ser Met Glu Ile Lys Met Ala Lys Asp Tyr Gly
          20          25          30
Phe Cys Phe Gly Val Lys Arg Ala Ile Gln Ile Ala Glu Lys Asn Gln

```

1246

```

225          230          235          240
Gln Thr Gly Phe Tyr Ala Pro His Lys Leu Leu Gly Gly Val Gly Gly
          245          250          255
Cys Gly Leu Leu Gly Ile Ser Lys Asp Leu Ile Asp Thr Gln Ile Pro
          260          265          270
Pro Ser Phe Ser Ala Gly Gly Val Ile Lys Tyr Ala Asn Arg Thr Arg
          275          280          285
His Glu Phe Ile Asp Glu Leu Pro Leu Arg Glu Glu Phe Gly Thr Pro
          290          295          300
Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
305          310          315
Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
          325          330          335
Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
          340          345          350
Asn Leu Thr Ala Ser Arg Val Gly Val Val Ala Phe Asn Ile Gly Gly
          355          360          365
Ile Ser Pro Tyr Asp Leu Ala Arg Val Leu Ser Tyr Glu Tyr Ala Ile
          370          375          380
Glu Thr Arg Ala Gly Cys Ser Cys Ala Gly Pro Tyr Gly His Asp Leu
385          390          395
Leu Asn Leu Asn Ala Gln Lys Ser Ser Asp Phe Asn Ala Lys Pro Gly
          405          410          415
Trp Leu Arg Val Ser Leu His Phe Thr His Ser Ile Asn Asp Ile Asp
          420          425          430
Tyr Leu Leu Asp Ser Leu Lys Lys Ala Val Lys Lys Leu Arg
          435          440          445

```

(2) INFORMATION FOR SEQ ID NO:1701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1701

```

Tyr Val Ile Glu Leu Asp Ile Asn Ala Ser Asp Lys Ser Leu Ser His
1          5          10          15
Arg Ala Val Ile Phe Ser Leu Leu Ala Gln Lys Pro Cys Phe Val Arg
          20          25          30
Asn Phe Leu Met Gly Glu Asp Cys Leu Ser Ser Leu Glu Ile Ala Gln
          35          40          45
Asn Leu Gly Ala Lys Val Glu Asn Thr Ala Lys Asn Ser Phe Lys Ile
          50          55          60
Thr Pro Pro Thr Thr Ile Lys Glu Pro Asn Lys Ile Leu Asn Cys Asn
65          70          75          80
Asn Ser Gly Thr Ser Met Arg Leu Tyr Ser Gly Leu Leu Ser Ala Gln
          85          90          95
Lys Gly Leu Phe Val Leu Ser Gly Asp Asn Ser Leu Asn Ala Arg Pro
          100          105          110
Met Lys Arg Ile Ile Glu Pro Leu Lys Ala Phe Gly Ala Lys Ile Leu
          115          120          125

```

[illegible]

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 446 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1700

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1244

210 215 220
 Ile Leu Glu Ser Lys Gly Ile
 225 230

(2) INFORMATION FOR SEQ ID NO:1699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...421

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1699

```

Met Lys Gly Leu Thr Met Lys Lys Leu Val Phe Ser Met Leu Leu Cys
1           5           10           15
Cys Lys Ser Val Phe Ala Glu Gly Glu Thr Pro Leu Ile Val Asn Asp
          20           25           30
Pro Glu Thr His Val Ser Gln Ala Thr Ile Ile Gly Lys Met Val Asp
          35           40           45
Ser Ile Lys Arg Tyr Glu Glu Ile Ile Ser Lys Ala Gln Ala Gln Val
          50           55           60
Asn Gln Leu Gln Lys Val Asn Asn Met Ile Asn Thr Thr Asn Ser Leu
65          70          75          80
Ile Ser Ser Ser Ala Ile Thr Leu Ala Asn Pro Met Gln Val Leu Gln
          85          90          95
Asn Ala Gln Tyr Gln Ile Glu Ser Ile Arg Tyr Asn Tyr Glu Asn Leu
          100         105         110
Lys Gln Ser Ile Glu Asn Trp Asn Ala Gln Asn Leu Leu Arg Asn Lys
          115         120         125
Tyr Leu Gln Gln Gln Cys Pro Trp Leu Asn Val Asn Ala Leu Thr Asn
          130         135         140
Asn Lys Ile Val Asn Leu Lys Asp Leu Asn Asn Leu Ile Thr Lys Asn
145         150         155         160
Gly Glu Gln Thr Gln Thr Ala Arg Asp Val Gln Asn Leu Ile Gln Ser
          165         170         175
Ile Ser Gly Ser Gly Tyr Gly Asn Met Gln Ser Leu Ala Gly Glu Leu
          180         185         190
Ser Gly Arg Ala Trp Gly Glu Met Leu Cys Lys Met Val Asn Asp Ser
          195         200         205
Asn Tyr Glu Ser Glu Gln Ala Leu Leu Ala Thr Gly Asn Asn Pro Glu
          210         215         220
Glu Gln Lys Arg Arg Phe Leu Leu Arg Val Lys Lys Val Asn Asp
225         230         235         240
Asn Lys Gln Leu Lys Asp Lys Leu Asp Pro Phe Leu Lys Arg Leu Asp
          245         250         255
Val Leu Gln Thr Glu Phe Gly Val Thr Asp Pro Thr Ala Asn His Asn
          260         265         270
Lys Gln Gly Ile His Tyr Cys Thr Glu Asn Lys Glu Thr Gly Lys Cys
          275         280         285
Asp Pro Ile Lys Asn Val Phe Arg Thr Thr Arg Leu Asp Asn Glu Leu
          290         295         300
Glu Gln Glu Ile Gln Thr Leu Thr Leu Asp Leu Thr Lys Ala Ser Asn
305         310         315         320

```

1243

Ala Met Ala Asn Met Ser Gly Glu Asn Asp Tyr Lys Ile Thr Trp Leu
 260 265 270
 Lys Pro Lys Tyr Gln Leu His Ser Ser Asn Asn Ile Lys Pro Leu Met
 275 280 285
 Ser Asn Thr Glu Leu Leu Asn Met Ile Glu Leu Thr Asn Ile Lys Lys
 290 295 300
 Glu Tyr Val Met Gly Cys Asn Met Glu Ile Asp Gly Ser Lys Tyr Pro
 305 310 315 320
 Ile His Lys Asp Trp Gly Phe Phe Gly Lys Ala Lys Val Pro Glu Thr
 325 330 335
 Trp Arg Asn Lys Ile Trp Glu Cys Ile Lys Asn Lys Val Lys Ser Tyr
 340 345 350
 Asp Asn Thr Thr Ala Glu Ile Gly Ile Val Trp Lys Lys Asn Thr Tyr
 355 360 365
 Ser Ile Ser His His
 370

(2) INFORMATION FOR SEQ ID NO:1698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1698

Lys Asp Tyr Lys Thr Lys Lys Arg Ala Ile Met Lys Thr Met Asn Leu
 1 5 10 15
 Asn Glu Phe Phe Thr His Lys Ile Ile Tyr Lys Asp Thr Pro Leu Lys
 20 25 30
 Phe Lys Asp Thr Leu Glu Gln Glu Ile Ser Gln Ala Ser Leu Val Glu
 35 40 45
 Lys Leu Ile Leu Ala Asn Ile Leu Ala Asn Met Val Phe Ala Lys Ile
 50 55 60
 Ser Asn Glu Asn Ala Pro Lys Ile Leu Ile Ser Arg Leu Met Cys Lys
 65 70 75 80
 Phe Ser Pro Ile Asp Tyr Glu Ser Thr Ile Pro Ser Asp Phe Lys Pro
 85 90 95
 Ile Asp Glu Glu Glu Tyr Glu Asp Asp Leu Glu Trp Leu Asn Glu Glu
 100 105 110
 Lys Glu Asp Arg Leu Phe Asn Tyr Tyr Leu Phe Leu Asn Gly Ile Lys
 115 120 125
 Glu Ser Asp Val Glu Glu Val Phe Asn Glu Ser Val Glu Ile Tyr Asp
 130 135 140
 Glu Cys Leu Ile Glu Ile Ala Gln Asn Val Leu Lys Asp Lys Phe Ser
 145 150 155 160
 Tyr Asp Ile Asp Leu Leu Gln Val Leu Val Lys Gly Tyr Ala Lys Glu
 165 170 175
 Ile Arg Glu Phe Leu Ser Tyr Lys Pro Ile Lys Glu Ile Lys Asp Phe
 180 185 190
 Lys Asp Lys Asp Thr Ala Leu Tyr Ile Ser Leu Gly Lys Asp Tyr Asp
 195 200 205
 Lys Glu Lys Glu Pro Phe Ser Lys Lys Leu Gln Gln Cys Phe Lys Glu

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1242

```

65          70          75          80
Ile Ala Phe Ser Pro Cys Val Ile Lys Glu Leu Asn Glu Phe Leu Leu
          85          90          95
Glu Phe Gly Ser Phe Lys Glu Thr Arg Ser Thr Phe Ile Glu Glu Ala
          100          105          110
Leu Ile Arg His Leu Lys His Arg Lys Asn Thr Gln Glu Gln Lys Leu
          115          120          125
Leu Lys Gln Leu Glu Arg Leu Gln Asn Lys Glu Lys Gly Asn Asn Glu
          130          135          140
Asn Asn Glu Leu Glu
145

```

(2) INFORMATION FOR SEQ ID NO:1697:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1697

```

Leu Asn Thr Asp Lys Ile Thr Lys Tyr Leu Ile Ile Ile Asp Ile Phe
1          5          10          15
Leu Lys Leu Tyr Val Ile Met Ile Ser Glu Ile Ile Lys Phe Gln Leu
          20          25          30
Lys Gly Ile Lys Met Ile Arg Leu Lys Gly Leu Asn Lys Thr Leu Lys
          35          40          45
Thr Ser Leu Leu Ala Gly Val Leu Leu Gly Ala Thr Ala Pro Leu Met
          50          55          60
Ala Lys Pro Leu Leu Ser Asp Glu Asp Leu Leu Lys Arg Val Lys Leu
          65          70          75          80
His Asn Ile Lys Glu Asp Thr Leu Thr Ser Cys Asn Ala Lys Val Asp
          85          90          95
Gly Ser Gln Tyr Leu Asn Ser Gly Trp Asn Leu Ser Lys Glu Phe Pro
          100          105          110
Gln Glu Tyr Arg Glu Lys Ile Phe Glu Cys Val Glu Glu Lys His
          115          120          125
Lys Gln Ala Leu Asn Leu Ile Asn Lys Glu Asp Thr Lys Asp Lys Glu
          130          135          140
Glu Leu Ala Lys Lys Ile Lys Glu Ile Lys Glu Lys Ala Lys Val Leu
          145          150          155          160
Arg Gln Lys Phe Met Ala Phe Glu Met Lys Glu His Ser Lys Glu Phe
          165          170          175
Pro Asn Lys Lys Gln Leu Gln Thr Met Leu Glu Asn Ala Phe Asp Asn
          180          185          190
Gly Ala Glu Ser Phe Ile Asp Asp Trp His Glu Arg Phe Gly Gly Ile
          195          200          205
Ser Arg Glu Asn Thr Tyr Lys Ala Leu Gly Ile Lys Glu Tyr Ser Asp
          210          215          220
Glu Gly Lys Ile Leu Ala Phe Gly Glu Arg Ser Tyr Ile Arg Gln Tyr
          225          230          235          240
Lys Lys Asp Phe Glu Ser Thr Tyr Asp Thr Arg Gln Thr Leu Ser
          245          250          255

```

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1241

Gln Asn Asn Asp Asn Ile Ile Ile Gln Ile
435 440

(2) INFORMATION FOR SEQ ID NO:1695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1695

```

Ile Lys His Tyr Lys Gln Tyr Gly Thr Gly Leu His Leu Phe Arg His
1           5           10           15
Ser Phe Ala Thr Leu Ile Tyr Gln Glu Thr Gln Asp Leu Val Leu Thr
          20           25           30
Ser Arg Ala Leu Gly His Ser Ser Leu Leu Ser Thr Lys Ile Tyr Ile
          35           40           45
His Thr Thr Gln Glu His Asn Lys Lys Val Ala Leu Val Phe Asp Ser
          50           55           60
Leu Ile Glu Asn Lys Lys
65           70

```

(2) INFORMATION FOR SEQ ID NO:1696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1696

```

Lys Lys Arg Lys Tyr Met Arg Phe Arg Arg Val Lys Lys His Lys Asn
1           5           10           15
Lys His Asn Lys Glu His Thr Ser Met Asp Leu Gln Gln Ile Asp Glu
          20           25           30
Leu Glu Lys Lys Phe Glu Glu Gln Glu Glu Gln Ala Gln Asp Thr Pro
          35           40           45
Leu Lys Gln Glu Pro Ser Thr Lys Glu Val Lys Ile Pro Lys Lys Arg
          50           55           60
Gly Arg Lys Lys Ser Leu Leu Asp Glu Asp Lys Lys Lys Ser Phe Asn

```

1240

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1694

```

Lys Glu Gln Gln Met Ala Tyr Lys Pro Asn Lys Lys Lys Leu Lys Glu
1      5      10      15
Leu Arg Glu Gln Pro Asn Leu Phe Ser Ile Leu Asp Lys Gly Asp Val
20      25      30
Ala Thr Asn Asn Pro Val Glu Glu Ser Asp Lys Ala Asn Lys Ile Gln
35      40      45
Glu Pro Leu Pro Tyr Val Val Lys Thr Gln Ile Asn Lys Ala Ser Met
50      55      60
Ile Ser Arg Asp Pro Ile Glu Trp Ala Lys Tyr Leu Ser Phe Glu Lys
65      70      75      80
Arg Val Tyr Lys Asp Asn Ser Lys Glu Asp Val Asn Phe Phe Ala Asn
85      90      95
Gly Glu Ile Lys Glu Ser Ser Arg Val Tyr Glu Ala Asn Lys Glu Gly
100     105     110
Phe Glu Arg Arg Ile Thr Lys Arg Tyr Asp Leu Ile Asp Arg Asn Ile
115     120     125
Asp Arg Asn Arg Glu Phe Phe Ile Lys Glu Ile Glu Ile Leu Thr His
130     135     140
Thr Asn Ser Leu Lys Glu Leu Lys Glu Gln Gly Leu Glu Ile Gln Leu
145     150     155     160
Thr His His Asn Glu Thr His Lys Lys Ala Leu Glu Asn Gly Asn Glu
165     170     175
Ile Val Lys Glu Tyr Asp His Leu Lys Asp Ile Tyr Gln Glu Val Glu
180     185     190
Arg Thr Lys Asp Gly Gly Leu Val Arg Glu Ile Ile Pro Ser Ile Ser
195     200     205
Ser Ala Glu Tyr Phe Lys Leu Tyr Asn Lys Leu Pro Phe Glu Ser Ile
210     215     220
Asn Asn Glu Asn Thr Lys Leu Asn Thr Asn Asp Asn Glu Glu Val Lys
225     230     235     240
Lys Leu Glu Phe Glu Leu Ala Lys Glu Val His Ile Leu Ile Leu Glu
245     250     255
Gln Gln Leu Leu Ser Ala Thr Asn Tyr Ser Trp Ile Asp Lys Asp
260     265     270
Asp Asn Ala Asn Phe Ala Trp Lys Met His Arg Leu Ile Asn Glu Asn
275     280     285
Lys Leu Lys Glu Asn His Leu Ser Ala Asn Asn Ala Asn Lys Ile Lys
290     295     300
Gln Phe Phe Phe Asn Asn Gly Ser Ile Leu Gly Trp Thr Lys Glu Glu
305     310     315     320
Gln Ser Ala Ile Gln Glu Asn Arg Asp Tyr Ser Leu Arg Ser Ala Leu
325     330     335
Leu Ser Leu Glu Glu Ile Ala Gln Ala Lys Ile Glu Leu Gln Lys Tyr
340     345     350
Tyr Glu Ser Val Tyr Val Asn Gly Asp Gly Asn Lys Arg Glu Ile Lys
355     360     365
Pro Phe Lys Glu Ile Leu Arg Asp Thr Asn Asn Phe Glu Lys Ala Tyr
370     375     380
Lys Glu Arg Tyr Asp Lys Leu Val Ser Leu Ser Ala Ala Ile Ile Gln
385     390     395     400
Ala Lys Glu Gly Gly Asn Glu Arg Gln Asn Ser Ser Ala Asn Asn Asn
405     410     415
Asn Pro Ile Lys Asn Thr Ile Glu Thr Asn Thr Ser Asn Asn Ile Ile
420     425     430

```

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```

Arg Glu Gly Ala Met Asn Phe Phe Asp Thr Leu Met Gly Met Phe Val
1      5      10      15
Glu Pro Ser Gln Lys Val Ala Lys Ser Leu Ala Glu His Val Gly Ser
20      25      30
Phe Phe His Ala Gln Leu Ile Leu Asn Thr Ile Ile Thr Ile Leu Phe
35      40      45
Met Ile Trp Ala Tyr Lys Arg Val Lys Glu Gly Asp Met Phe Glu Phe
50      55      60
Lys Thr Ala Met Gly Val Val Val Phe Ile Ala Phe Val Gly Phe Ile
65      70      75      80
Asn Trp Gly Ile Lys Asn Pro Asn Asp Phe Asn Thr Tyr Phe Ile Asn
85      90      95
Thr Ile Phe Tyr Pro Ser Glu Lys Leu Ala Ile Leu Ile Ala Gln Ser
100     105     110
Leu Asn Asp Gly Leu Glu Ile Pro Thr Asn Thr Asn Leu Ser Pro Ser
115     120     125
Glu Ile Phe Ser Ile Gly Asn Leu Ala Ser Ser Ala Tyr Ala Met Ile
130     135     140
Val Asn Leu Trp Asp Asn Ala Phe Asp Gly Ile Asn Met Phe Asn Trp
145     150     155     160
Leu Thr Met Ile Pro Lys Ile Ile Met Phe Phe Leu Val Ile Leu Gly
165     170     175
Glu Leu Leu Phe Leu Gly Leu Leu Leu Ile Ile Val Leu Leu Val Thr
180     185     190
Ala Glu Ile Phe Met Trp Ser Ala Leu Gly Leu Ile Val Leu Pro Leu
195     200     205
Gly Leu Ile Pro Gln Thr Lys Gly Met Leu Phe Ser Tyr Leu Lys Lys
210     215     220
Leu Ile Ser Leu Thr Leu Tyr Lys Pro Cys Met Met Leu Val Ala Phe
225     230     235     240
Phe Asn Tyr Gly Ile Ile Tyr Lys Val Asn Thr Leu Ile Pro Thr Lys
245     250     255
His Glu Val Thr Gln Gly Phe Tyr Gly Asn Ala Asp Lys Met Ala Asn
260     265     270
Glu Gly Lys Ile Ile Asp Val Phe Gly Asn Val Leu Lys Gly Asp Trp
275     280     285
Asn Ser Tyr Ile Ala His Ser Ser Ile Val Gly Phe Leu Thr Ile Ile
290     295     300
Val Leu Gly Ser Val Ile Cys Phe Phe Leu Val Lys Arg Val Pro Asp
305     310     315     320
Phe Ile Asn Asn Ile Phe Gly Thr Ser Gly Gly Val Gly Ala Val Thr
325     330     335
Glu Met Met Gln Lys Ile Gly Met Thr Ile Gly Gly Ala Val Phe Gly
340     345     350
Gly Ser Ala Val Met Val Ala Asn Gln Val Lys Gln Ala Tyr Gln Ser
355     360     365
Ala Gly Gly Gly Leu Ala Gly Leu Gln Ala Gly Ala Lys Ala Phe Gly
370     375     380
Leu Gly Ala Ile Ser Gly Gly Ala Ser Ala Met Ala Asn His Arg Ser
385     390     395     400
Val Lys Ala Gly Val Lys His Phe Val Ala Ser Val Lys Ser Gly Phe
405     410     415
Gly Phe Asp Asn Asp Lys Asn Asn Lys
420     425

```

(2) INFORMATION FOR SEQ ID NO:1694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1238

2100	2105	2110
Asn Glu Glu Ser Leu Lys	Asn Asn Ala Ser Lys Leu Asp Tyr Leu Lys	
2115	2120	2125
Gln Glu Leu Lys Asp Leu Glu Thr Leu Gln Arg Ser Val Ile Ile Pro		
2130	2135	2140
Thr His Thr Glu Ile Lys Leu Tyr Asp Leu Lys Asn Glu Glu Ser Lys		
2145	2150	2155
Asp Tyr Glu Leu Ile Lys Val Lys Glu Val Glu Pro Leu Lys Glu Asn		2160
2165	2170	2175
Ala Ser Met Ser Glu Glu Leu Thr His Lys Lys Leu Lys Glu Gln Asn		
2180	2185	2190
Lys Gln Ile Ala Glu Gln Asn Lys Glu Lys Leu Asp Ala Ile Lys Lys		
2195	2200	2205
Gln Phe Ala Ser Asn Leu Asn Thr Leu Phe Val Asn Glu Glu Glu Asp		
2210	2215	2220
Tyr Lys Leu Leu Glu Tyr Lys Gly Phe Val Val Asn Ala Tyr Lys Thr		
2225	2230	2235
Lys Tyr Gln Val Glu Phe Ser Leu Ser Pro Lys Asp Asn Pro Asn Ile		2240
2245	2250	2255
Ala Tyr Ser Pro Ser Asn Met Val Tyr Lys Asn Asp Thr Ile Asn Met		
2260	2265	2270
Phe Ser Ser Tyr Asn Phe Cys Ala Glu Ile Lys Phe Asp Gly Phe Leu		
2275	2280	2285
Lys Arg Leu Asp Asn Ala Ile Thr Lys Leu Pro Glu Lys Ile Lys Glu		
2290	2295	2300
Leu Glu Asn Ser Ile Glu Ile Thr Lys Lys Asn Ile Ala Lys Tyr Thr		
2305	2310	2315
Arg Leu Val Glu Gln Lys Pro Ser Tyr Pro Arg Leu Glu Tyr Leu Gln		
2325	2330	2335
Ala Leu Lys Trp Asp His Lys Thr Leu Ile Asp Asp Leu Ala Lys Met		
2340	2345	2350
Ser Lys Asp Arg Asn Tyr Lys Pro Ala Phe Asn Pro Lys Ser Lys Glu		
2355	2360	2365
Val Leu Lys Asn Leu Asn Ala Glu Lys Arg Ala Ser Leu Glu Asn Glu		
2370	2375	2380
Arg Glu Glu Gln Gly Val Lys Gly Asn Thr Lys Ser His Asp Glu Ile		
2385	2390	2395
Glu Pro Ala Thr Glu Gln Val Ile Glu Lys Glu Ile Glu Lys Gly Asp		2400
2405	2410	2415
Glu Ile Ala Asn Val Asp Tyr Tyr Glu Asn Glu Gln Glu Val Glu		
2420	2425	2430
Ile Thr Lys Ser Met Gly Arg Arg		
2435	2440	

(2) INFORMATION FOR SEQ ID NO:1693:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 425 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1693

SUBSTITUTE SHEET (RULE 26)

1237

Val Asp Glu Ala His Leu Phe Lys Asn Leu Ala Phe Glu Thr Ser Met
 1585 1590 1595 1600
 Glu Lys Ile Ala Gly Leu Gly Asn Gln Gln Gly Ser Asn Arg Ala Arg
 1605 1610 1615
 Asp Leu Phe Ile Lys Thr Arg Tyr Leu His Gln Asn Asp Lys Lys Ile
 1620 1625 1630
 Met Phe Leu Thr Gly Thr Pro Ile Ala Asn Ser Leu Ser Glu Met Tyr
 1635 1640 1645
 His Leu Gln Arg Tyr Leu Thr Pro Asp Val Leu Lys Glu Arg Gly Leu
 1650 1655 1660
 Glu Phe Phe Asp Asp Trp Ala Lys Thr Tyr Gly Glu Val Val Asn Asp
 1665 1670 1675 1680
 Phe Glu Leu Asp Thr Ser Ala Gln Ser Tyr Lys Met Val Asn Arg Phe
 1685 1690 1695
 Ser Lys Phe Ser Asp Val Gln Gly Leu Ser Thr Met Tyr Arg Ala Phe
 1700 1705 1710
 Ala Asp Ile Val Ser Asn Asp Asp Ile Leu Lys His Asn Pro His Phe
 1715 1720 1725
 Val Pro Lys Val Tyr Gly Asp Lys Pro Ile Asn Val Val Val Lys Arg
 1730 1735 1740
 Ser Glu Glu Val Ala Gln Phe Ile Gly Val Ala Leu Glu Asn Gly Lys
 1745 1750 1755 1760
 Tyr Asn Glu Gly Ser Ile Ile Asp Arg Met Gln Lys Cys Glu Gly Lys
 1765 1770 1775
 Lys Ser Gln Lys Gly Gln Asp Asn Ile Leu Ser Cys Thr Thr Asp Ala
 1780 1785 1790
 Arg Lys Val Ala Leu Asp Tyr Arg Leu Ile Asp Pro Asn Ala Lys Val
 1795 1800 1805
 Glu Lys Glu Phe Ser Lys Ser Tyr Ala Met Ala Lys Asn Ile Tyr Glu
 1810 1815 1820
 Asn Tyr Leu Glu Thr His Ala Thr Lys Gly Thr Gln Leu Gly Phe Ile
 1825 1830 1835 1840
 Gly Leu Ser Thr Pro Lys Thr His Ser Gln Lys Val Ser Leu Glu Ala
 1845 1850 1855
 Leu Asp Asn Ala His Glu Thr Glu Asn Lys Asn Pro Leu Asp Lys Ala
 1860 1865 1870
 Gln Glu Leu Glu Ser Leu Ser Ser Tyr Asp Glu Lys Gly Asn Leu
 1875 1880 1885
 Ile Ala Pro Ser Lys Lys Glu Leu Glu Asn Glu Leu Lys Glu Lys Glu
 1890 1895 1900
 Ala Lys Ser Val Asn Leu Asp Glu Glu Ile Ala Lys Gly Cys Ser Phe
 1905 1910 1915 1920
 Asp Val Tyr Ser Asp Val Leu Arg His Leu Val Gln Met Gly Ile Pro
 1925 1930 1935
 Gln Asn Glu Ile Ala Phe Ile His Asp Ala Lys Thr Glu Glu Gln Lys
 1940 1945 1950
 Gln Asp Leu Phe Lys Lys Leu Asn Arg Gly Gly Val Arg Val Leu Leu
 1955 1960 1965
 Gly Ser Pro Ala Lys Met Gly Val Gly Thr Asn Val Gln Glu Arg Leu
 1970 1975 1980
 Val Ala Met His Glu Leu Asp Cys Pro Trp Arg Pro Asp Glu Leu Leu
 1985 1990 1995 2000
 Gln Met Glu Gly Arg Gly Ile Arg Gln Gly Asn Ile Leu His Gln Asn
 2005 2010 2015
 Asp Pro Glu Asn Phe Arg Met Lys Ile Tyr Arg Tyr Ala Thr Glu Lys
 2020 2025 2030
 Thr Tyr Asp Ser Arg Met Trp Gln Ile Ile Glu Thr Lys Ser Lys Gly
 2035 2040 2045
 Ile Glu Gln Phe Arg Asn Ala His Lys Leu Gly Leu Asn Glu Leu Glu
 2050 2055 2060
 Asp Phe Asn Met Gly Ser Ser Asn Ala Ser Glu Met Lys Ala Glu Ala
 2065 2070 2075 2080
 Thr Gly Asn Pro Leu Ile Ile Glu Glu Val Lys Leu Arg Ala Glu Ile
 2085 2090 2095
 Lys Ser Glu Glu Ser Lys Tyr Lys Ala Phe Asn Lys Glu His Tyr Phe

SUBSTITUTE SHEET (RULE 26)

1236

1060 1065 1070
 Asp Phe Glu Lys Glu Ile Thr Pro Arg Ser Ala Lys Met Gln Asn Ile
 1075 1080 1085
 Glu Pro Arg Gln Ala Gln Ala Lys Lys Ala Gln Ile Phe Phe Glu Arg
 1090 1095 1100
 Thr Leu Asn Pro Lys Lys Glu Leu Ile Ile Thr Asn Ala Lys Glu Ala
 1105 1110 1115 1120
 Leu Ile Ala Ser Ile Asn Gln Lys Gly Gly Leu Asp Leu His Phe Ile
 1125 1130 1135
 Arg Asp His Phe Thr Thr Gln Ser Leu Glu Thr Thr Ile Lys Glu Leu
 1140 1145 1150
 Leu Glu Gln Lys Leu Ile Tyr Lys Asp His Lys Asp Asn Gly Gly Tyr
 1155 1160 1165
 Ile Leu Ala Asn Asp Tyr Leu Ser Gly Asn Val Lys Arg Lys Leu Lys
 1170 1175 1180
 Glu Val Lys Glu Ala Ile Asn Gln Gly Val Glu Gly Leu Glu Ala Asn
 1185 1190 1195 1200
 Val Lys Asp Leu Glu Leu Ile Ile Pro Lys Asp Leu Lys Ala Thr Glu
 1205 1210 1215
 Ile Met Ala Asn Ile Asn Ser Pro Trp Ile Pro Thr Gln Tyr Leu Glu
 1220 1225 1230
 Glu Phe Leu Met Glu Leu Ser Ala Asn His Tyr Glu Lys Gln Tyr Gly
 1235 1240 1245
 Asp Lys Met Thr Asp Tyr Gln Leu Ser Asn Leu Lys Glu Asp Ile Lys
 1250 1255 1260
 Ile Glu His Leu Ser Gly Ala Tyr Glu Val Phe Val Arg Asn Asn Glu
 1265 1270 1275 1280
 Leu Asn Glu Leu Tyr Gly Ile Arg His Lys Asp Lys Pro His Ser Tyr
 1285 1290 1295
 Lys Val Pro Phe Glu Ser Leu Leu Asn Lys Val Leu Asn Asn Lys Asp
 1300 1305 1310
 Leu Ser Val Lys Tyr Ala Gln Val Asp Pro Asn Asp Pro Lys Lys Glu
 1315 1320 1325
 Ile Phe Ile Thr Asp Glu Glu Gln Ser Asn Leu Ala Arg Gln Lys Ala
 1330 1335 1340
 Glu Glu Leu Lys Glu Ala Phe Lys Asp Trp Ile Tyr Lys Asp Tyr Ser
 1345 1350 1355 1360
 Arg Arg Thr His Leu Glu Gln Ile Tyr Asn Asp Thr Phe Asn Asn Phe
 1365 1370 1375
 Val Leu Lys Thr Tyr Asp Gly Ser Gln Leu Glu Leu Glu Gly Phe Asn
 1380 1385 1390
 Tyr His Ile Ser Leu Arg Pro His Gln Lys Asn Ala Ile Phe Arg Thr
 1395 1400 1405
 Ile Gln Asp Arg Ala Val Cys Leu Asp His Gln Val Gly Ala Gly Lys
 1410 1415 1420
 Thr Leu Cys Ala Ile Ala Ser Cys Met Glu Gln Lys Arg Met Gly Leu
 1425 1430 1435 1440
 Val Asn Lys Thr Leu Ile Ala Val Pro Asn His Leu Thr Lys Gln Trp
 1445 1450 1455
 Gly Asp Glu Phe Tyr Lys Ala Tyr Pro Asn Ala Asn Val Leu Val Val
 1460 1465 1470
 Asp Ser Lys Asp Thr Thr Glu Lys Glu Arg Glu Leu Leu Phe Asn Gln
 1475 1480 1485
 Ile Ala Asn Asn Asn Tyr Asp Ala Val Val Ile Ala His Thr His Leu
 1490 1495 1500
 Glu Leu Leu Ser Asn Pro Arg Gly Ile Ile Glu Glu Leu Lys Glu Glu
 1505 1510 1515 1520
 Glu Leu Val Asn Ala Glu Lys Asn Phe Glu Arg Gln Glu Leu Ala Tyr
 1525 1530 1535
 Lys Asn Asn Pro Arg Glu Thr Lys Lys Pro Asn Glu Arg Ala Phe Lys
 1540 1545 1550
 Asn Lys Leu Asp Lys Ile Arg Ala Lys Tyr Asp Ala Ile Leu Glu Lys
 1555 1560 1565
 Gln Gly Ser His Ile Asp Ile Ser Gln Met Gly Ile Asp Asn Leu Ile
 1570 1575 1580

SUBSTITUTE SHEET (RULE 26)

1235

Leu Glu Ser Tyr Phe Lys Lys Ala Gln His Pro Glu Glu Phe Lys Glu
 545 550 555 560
 Leu Asn Ala Leu Leu Thr Lys Asp Glu Phe Arg Arg Ala Tyr Leu Ser
 565 570 575
 Ala Arg Asp Ala Tyr Tyr Thr Pro Lys Leu Val Ile Asp Ser Ile Tyr
 580 585 590
 Gln Gly Leu Asp Gln Leu Gly Phe Asn Asn Asp Asn His Pro Lys Lys
 595 600 605
 Ile Phe Glu Pro Ser Leu Gly Thr Gly Lys Phe Ile Ala His Ala Pro
 610 615 620
 Ser Asp Lys Asn Tyr Arg Phe Ile Gly Thr Glu Leu Asp Pro Ile Ser
 625 630 635 640
 Ala Asn Leu Ser Lys Phe Leu Tyr Pro Asn Gln Val Ile Gln Asn Thr
 645 650 655
 Ala Leu Glu Asn Tyr Gln Phe Tyr Gln Glu Tyr Asp Ala Phe Val Gly
 660 665 670
 Asn Pro Pro Tyr Gly Asn His Lys Ile Tyr Ser Ser Asn Asp Lys Glu
 675 680 685
 Leu Ser Asn Glu Ser Ile His Asn Tyr Phe Leu Gly Lys Ala Ile Lys
 690 695 700
 Glu Leu Lys Asp Asp Gly Ile Gly Ala Phe Val Val Ser Ser Trp Phe
 705 710 715 720
 Met Asp Ala Lys Asn Pro Lys Met Arg Glu His Ile Ala Lys Asn Ala
 725 730 735
 Thr Phe Leu Gly Ala Ile Arg Leu Pro Asn Ser Val Phe Lys Ala Thr
 740 745 750
 Gly Ala Glu Val Thr Ser Asp Ile Val Phe Phe Lys Lys Gly Val Glu
 755 760 765
 Lys Ala Thr Asn Gln Ser Phe Thr Lys Ala Met Pro Tyr Tyr Asp Lys
 770 775 780
 Ile Leu Asn Ser Leu Asp Asp Asp Thr Leu Phe Ala Leu Gln Asn Asn
 785 790 795 800
 Arg Phe Asp Ser Phe Ile Pro Ser Asp Gln Leu Lys Ile Val Asn Ala
 805 810 815
 Val Ala Asn His Phe Gly Phe Lys Gln Glu Lys Leu Gln Arg Trp Tyr
 820 825 830
 Glu Lys Ile Asp Thr Ala Asn Phe Gly Tyr Ser Thr Gln Asp Tyr Lys
 835 840 845
 Ile Ile Lys Asp Phe Ile Asp Lys Val Gly Lys Asn Ser Ile Asn Leu
 850 855 860
 Asn Glu Gln Thr Leu Asn Glu Tyr Phe Ile His His Pro Glu Asn Ile
 865 870 875 880
 Leu Gly His Leu Ser Leu Glu Lys Thr Arg Tyr Arg Phe Glu Thr Asn
 885 890 895
 Gly Glu Gln Ile Tyr Lys Tyr Asp Leu Gln Ala Leu Glu Asp Glu Ser
 900 905 910
 Leu Asp Leu Ser Gln Ala Leu Lys Gln Ala Ile Glu Lys Leu Pro Lys
 915 920 925
 Asp Val Tyr Gln Tyr His Lys Thr Thr Leu Lys Thr Asp Val Leu Ile
 930 935 940
 Ile Asp Ser Ser Asn Glu Arg Tyr Gln Glu Val Gln Lys Leu Ile Lys
 945 950 955 960
 Asn Leu Glu Arg Arg Glu Leu Val Lys Trp Asp Asn Leu Tyr Phe Gln
 965 970 975
 Leu Glu Gln Asn Asn Glu Met Gly Ile Phe Leu Lys Pro Thr Lys Ile
 980 985 990
 Asn Ser Lys Val Gln Asp Ser Arg Leu Lys Ala Tyr Phe Lys Ile Lys
 995 1000 1005
 Asp Ala Leu Asn Asp Leu Thr Ser Ala Glu Leu Asn Pro Leu Ser Ser
 1010 1015 1020
 Asp Leu Glu Leu Glu Asn Lys Arg Ala Lys Leu Asn Leu Val Tyr Asp
 1025 1030 1035 1040
 Glu Phe Val Lys Lys Phe Gly Tyr Leu Asn Glu Asn Lys Asn Arg Lys
 1045 1050 1055
 Asp Ile Arg Gln Asp Leu Tyr Gly Ala Lys Val Leu Gly Leu Glu Lys

1234

20 25 30
 Pro Asn Gly Thr Arg Ala Gly Ile Pro Gln Glu Ile His Arg Arg Ser
 35 40 45
 Glu Pro Arg Gly Gln Gln Glu Gly Met Glu Arg Ser Ser Asp Glu Asp
 50 55 60
 Leu Ser His Gln Asp Pro Ser Leu Phe Ile Glu Ser Arg Glu Gln Gly
 65 70 75 80
 Gly Thr Arg Gly Val Tyr Arg Ser Ser Asp Gln Gln Ala Val Ser Glu
 85 90 95
 Glu Ser His Arg Glu Arg Asp Arg Ile His Glu His Val Ser Arg Gly
 100 105 110
 Asp Gly Val Ser Ala Arg Ala Asp Ala Arg Ala Asn Ser Asn Gly Ala
 115 120 125
 Ser Ser Pro Ala Ser Arg Met Glu Asn Gly Ala Arg Ser Glu Glu Lys
 130 135 140
 Gly Asp Asn Pro Ser Asp Glu Arg Gly Ile Pro Gln Thr Pro Gln Ser
 145 150 155 160
 Pro Ser His Gln Gln Asn Ser Ser Arg Asp Leu Gly Leu Ser Leu Ser
 165 170 175
 Arg Glu Gln Pro Gly Gln Thr Gly Arg Leu Arg Leu Phe Asp His Gly
 180 185 190
 Gln Met Gly Ser Leu Phe Pro Thr Asp His Glu Asn Gln Arg Lys Arg
 195 200 205
 Ser Asp Asn Glu Leu Asp Arg Arg Ser Asp Lys Ala Asn Glu Asn Gly
 210 215 220
 Asp Lys Ser Pro Arg Gln Asn Gly Ser Ala Asn Gln Glu Ser Ala Arg
 225 230 235 240
 Ser Glu Arg Tyr Gly Ile Ala Gln Gly Ser Ser Asn Gln Ser Val Leu
 245 250 255
 Leu Pro Ala Gln Ser Arg Leu His His Ala Gly Leu Ser Ala Gln Asn
 260 265 270
 Gly Leu Arg Asp Leu Glu Glu Asn Arg Asp Gln Glu Gly Arg Leu Leu
 275 280 285
 Ser Asn Leu Asp Asn Leu Glu Ser Leu Leu Asn Ala Ile Arg Asn Asn
 290 295 300
 Thr Ile Ala Ser Glu Pro Asp Phe Arg Ser Arg Leu Leu Glu Ala Ile
 305 310 315 320
 Gln Asn Asn Asp Pro Leu Lys Asp Ser Ile Val Gly Ala Gln Leu Leu
 325 330 335
 Lys Asp Pro Thr Lys Lys Ile Phe Tyr Asp Lys Phe Gln Leu Lys Ile
 340 345 350
 Ser Pro Lys Lys Val Leu Glu Ile Leu Glu Asn Arg Leu Lys Lys Ser
 355 360 365
 Ile Glu Thr Thr Asn Glu Thr Leu Asn Ala Phe Asn Val Leu Asp Ser
 370 375 380
 Gln Ala Ile Asp Leu Asn Ala Ile Ser Asn Ser Val Gly Leu Asn Pro
 385 390 395 400
 Thr Gln Glu Ser Lys Ile Thr Asp Asn Ser Val Glu Leu Asn Asn Ala
 405 410 415
 Gln Glu Gln Thr Ala Gln Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln
 420 425 430
 Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu
 435 440 445
 Gln Thr Thr Gln Glu Gln Thr Thr Gln Glu Gln Asp Thr Gln Glu Asn
 450 455 460
 Ala Pro Thr Thr Ile Lys Gln Glu Thr Pro Ile Thr Pro Ala Ile Pro
 465 470 475 480
 Leu Asn Pro Lys Ile Asp Phe Lys Pro Ser Glu Glu Val Leu Ile Lys
 485 490 495
 Gly Ala Lys Thr Arg Tyr Lys Ala Asn Ile Lys Ala Ile Glu Leu Leu
 500 505 510
 Lys Glu Leu Gln Ala Lys Gln Glu Ile Leu Lys Gly Asp Tyr Tyr Ala
 515 520 525
 Thr Leu Lys Glu Gln Glu Ile Leu Ala Gln Phe Ser Gly Trp Gly Gly
 530 535 540

1233

Thr Leu Ser Ser Leu Val Arg Ala Phe Leu Glu Ser Ile Ala Lys Asn
 405 410 415
 Leu Met Val Lys Glu Ser Ser Lys Pro Glu Glu Arg Ile Phe Ile Ile
 420 425 430
 Ala Asp Glu Phe Val Arg Phe Gly Lys Leu Pro Phe Leu Leu Glu Met
 435 440 445
 Pro Ala Leu Cys Arg Ser Tyr Asn Val Val Pro Leu Phe Ile Thr Gln
 450 455 460
 Asp Tyr Ala Met Ile Arg Lys Tyr Tyr Ser Asp Asp Asp Leu Lys Ile
 465 470 475 480
 Leu Lys Gly Val Val His Tyr Asn Ile Val Phe Lys Met Asn Ser Ala
 485 490 495
 Glu Asp Ala Glu Ile Val Ser Lys Glu Val Gly Glu Phe Thr Arg Arg
 500 505 510
 Ser Lys Asn Tyr Ser Thr Glu Lys Gly Gln Leu Val Phe Gly Gly Ser
 515 520 525
 Ser Ser Tyr Ser His Glu Gly Arg Asn Leu Leu Thr Ala Gln Asp Ile
 530 535 540
 Met Asn Ile Asn Ser Asp Glu Val Ile Val Ile Val Thr Gly Ala Lys
 545 550 555 560
 Ala Thr Pro Leu Lys Leu Lys Ala Asn Tyr Trp Phe Lys Asp Lys Glu
 565 570 575
 Leu Leu Lys Arg Ala Asn Leu Pro Ile Asp Leu Glu Val Glu Arg Gln
 580 585 590
 Arg Val Glu Glu Pro Ile Gln Pro Thr Thr Glu Ile Glu Thr Thr Pro
 595 600 605
 Asn Gln Asn Lys Ala Asp Leu Glu Pro Ser Asn Lys Gly Glu Lys Val
 610 615 620
 Glu Asn Glu Ser Asn Glu Arg Asn Thr Asn Glu Asn Asn Pro Thr Thr
 625 630 635 640
 Pro Gln Glu Leu Glu Asn Ser Asn Leu Lys Glu Ser Glu Lys Asp Asn
 645 650 655
 Glu Ser Pro Ile Thr Leu Glu Asn Ala Asn Glu Asn Ile Glu Gln Gly
 660 665 670
 Asn His Asn Glu Ile Asp Glu Ile Leu Lys Lys Pro Leu Ser Glu Ile
 675 680 685
 Ser Met Glu Glu Lys Arg Ala Leu Phe Lys Lys Met Gln Gln Ser Asp
 690 695 700
 Glu Glu Ser Glu Gln Glu Val Thr Gln Ser Thr Gln Ser
 705 710 715

(2) INFORMATION FOR SEQ ID NO:1692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2440 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...2440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1692

Tyr Asn His Pro Asn Leu Ser Val Ala Asp Leu Glu Leu Glu Gln Gln
 1 5 10 15
 Asn Leu Gly Glu Gln Asn Gly Lys Glu Arg Thr Asn Arg Ala Asp Glu

SUBSTITUTE SHEET (RULE 26)

1232

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1691

```

Tyr Ala Leu Lys Ser Leu Arg Gln Ala Tyr Phe Phe Ser Gln Ser Val
1      5      10      15
Phe Val Gly Leu Tyr His Gly Ala Ser Ile Phe Asp Leu Lys Phe Glu
20     25     30
Val Tyr Leu Thr Met Leu Ile Ser Leu Met Pro Phe Val Ala Thr Ile
35     40     45
Tyr Ile Asn Phe Pro Lys Thr Thr Glu Thr Ser His Gly Tyr Ala Arg
50     55     60
Trp Ala Asn Val Lys Asp Ile Glu Cys Phe Lys Ile Phe Ser Lys Glu
65     70     75     80
Gly Phe Cys Lys Val Val His Arg Leu Gly Val Gln Phe Asp Asn Gly
85     90     95
Phe Ile Leu Gly Lys Phe Gly Phe Pro Lys Leu Arg Asn Val Cys Tyr
100    105    110
Asp Lys Pro Leu Gly Thr Met Ile Val Ala Pro Pro Gly Ala Gly Lys
115    120    125
Thr Ala Cys Val Ala Leu Pro Asn Leu Leu Thr Leu Pro Asn Ser Cys
130    135    140
Ile Ile Thr Asp Ile Lys Gly Glu Leu Arg Asp Lys Thr Ala Gly Tyr
145    150    155    160
Arg Gln Lys Phe Leu Asn Asn Arg Ile Leu Ile Phe Asn Pro Tyr Gly
165    170    175
Asp Asp Asn Thr Cys Tyr Phe Asn Pro Phe Asp Lys Arg Ile Val Glu
180    185    190
Lys Met Thr Phe Ala Glu Gln Leu Arg His Val Lys Ala Val Gly Asp
195    200    205
Gly Ile Phe Val Asp Glu Glu Asp His Trp Val Ser Lys Ala Lys Glu
210    215    220
Leu Phe Val Phe Phe Ala Leu Leu Gln Val Val Thr Lys Gly His Ser
225    230    235    240
Ser Phe Tyr Asp Val Ser Ile Ala Pro Ala Asn Asp Tyr Ala Pro Leu
245    250    255
Ile His Pro Lys Ser Pro Tyr Tyr Lys Gln Leu Tyr Gln His Asp Lys
260    265    270
Lys Thr Gly Glu Val Ile Leu Asp Pro Gln Thr Asn Ala Pro Met Lys
275    280    285
Asn Pro Gln Ala Asn Val Leu Lys Leu Phe Leu Asn Gln Val Ala Asp
290    295    300
Gln Lys Tyr Ile Asp Met Asn Asp Glu Lys Asn Tyr Asp Pro Arg Glu
305    310    315    320
Pro Glu Pro Pro Tyr Gly Thr Lys Gly Ala Leu Asp Glu Ile Ile Arg
325    330    335
Thr Asp Ala Arg Ser Trp Ala Asn Thr Pro Asp Asp Glu Phe Gly Ser
340    345    350
Ile Met Ser Ser Phe Lys Arg Phe Met Tyr Val Tyr Lys Asp Pro Lys
355    360    365
Val Arg Glu Ala Thr Ser Lys Met Ser Phe Asp Tyr Glu Glu Leu Arg
370    375    380
Thr Gly Asn Ile Ser Ile Tyr Ile Val Ile Ala Gln Ile Asp Ile Gly
385    390    395    400

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SUBSTITUTE SHEET (RULE 26)

1231

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1690

```

Val Phe Thr Pro Arg Val Lys Arg Phe Phe Ile Phe Leu Phe Leu Phe
1      5      10      15
Leu Ile Leu His Glu Ile Leu Asn Thr Glu Leu Ala Pro Leu Asn Gly
20      25      30
Ile Ser Leu Ala Leu Gly Tyr Leu Cys Leu Phe Ile Leu Val Leu Ser
35      40      45
Ala Ser Leu Ile Phe Glu Lys Val Leu Ser Lys Gln Tyr Leu Gln Thr
50      55      60
Ala Lys Asp Lys Ile Ala Ser Leu Lys Asn Leu Lys Val Ile Ala Ile
65      70      75      80
Thr Gly Ser Phe Gly Lys Thr Ser Thr Lys Asn Phe Leu His Gln Ile
85      90      95
Leu Gln Thr Gln Phe Asn Ala His Ala Ser Pro Lys Ser Val Asn Thr
100     105     110
Leu Leu Gly Ile Ala Asn Asp Ile Asn Gln Asn Leu Asp Asp Arg Ser
115     120     125
Glu Ile Tyr Ile Ala Glu Ala Gly Ala Arg Asn Lys Gly Asp Ile Lys
130     135     140
Glu Ile Thr Arg Leu Ile Glu Pro His Leu Ala Val Val Ala Glu Val
145     150     155     160
Gly Glu Gln His Leu Glu Tyr Phe Lys Thr Leu Glu Asn Ile Cys Glu
165     170     175
Thr Lys Ala Glu Leu Leu Asp Ser Lys Arg Leu Glu Lys Ala Phe Cys
180     185     190
Tyr Ser Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu
195     200     205
Ile Asp Tyr Ser Ser Leu Val Arg Asn Val Gln Ser Thr Leu Lys Gly
210     215     220
Thr Ser Phe Glu Thr Leu Ile Asn Gly Val Trp Glu Ser Phe Glu Thr
225     230     235     240
Lys Val Leu Gly Glu Phe Asn Ala Tyr Asn Ile Ala Ser Ala Ile Leu
245     250     255
Ile Ala Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val
260     265     270
Phe Glu Leu Lys Pro Ile Asn His Arg Leu Gln Leu Leu Glu Ala Asn
275     280     285
Gln Lys Ile Ile Ile Asp Asp Ser Phe Asn Gly Asn Leu Lys Gly Met
290     295     300
Leu Glu Gly Ile Arg Leu Ala Ser Leu His Gln Gly Arg Lys Val Ile
305     310     315     320
Val Thr Pro Gly Leu Val Glu Ser Asn Thr Glu Ser Asn Glu Ala Leu
325     330     335
Ala Gln Lys Ile Asp Gly Val Phe Asp Val Ala Ile Ile Thr Gly Glu
340     345     350
Leu Asn Ser Lys Thr Ile Ala Ser Lys Leu Lys Thr Pro Gln Lys Ile
355     360     365
Leu Leu Lys Asp Lys Ala Gln Leu Glu Asn Ile Leu Gln Ala Thr Thr
370     375     380
Ile Gln Gly Asp Leu Ile Leu Phe Ala Thr Asp Ala Pro Asn Tyr Ile
385     390     395     400

```

(2) INFORMATION FOR SEQ ID NO:1691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 amino acids

(B) TYPE: amino acid

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1230

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1689

```

Met Lys Gln Phe Lys Lys Lys Pro Lys Lys Ile Lys Arg Ser His Gln
 1           5           10           15
Asn Gln Lys Thr Ile Leu Lys Arg Pro Leu Trp Leu Met Pro Leu Leu
 20           25           30
Ile Gly Gly Phe Ala Ser Gly Val Tyr Ala Asp Gly Thr Asp Ile Leu
 35           40           45
Gly Leu Ser Trp Gly Glu Lys Ser Gln Lys Val Cys Val His Arg Pro
 50           55           60
Trp Tyr Ala Ile Trp Ser Cys Asp Lys Trp Glu Glu Lys Thr Gln Gln
 65           70           75           80
Phe Thr Gly Asn Gln Leu Ile Thr Lys Thr Trp Ala Gly Gly Asn Ala
 85           90           95
Ala Asn Tyr Tyr His Ser Gln Asn Asn Gln Asp Ile Thr Ala Asn Leu
100          105          110
Lys Asn Asp Asn Gly Thr Tyr Phe Leu Ser Gly Leu Tyr Asn Tyr Thr
115          120          125
Gly Gly Glu Tyr Asn Gly Gly Asn Leu Asp Ile Glu Leu Gly Ser Asn
130          135          140
Ala Thr Phe Asn Leu Gly Ala Ser Ser Gly Asn Ser Phe Thr Ser Trp
145          150          155          160
Tyr Pro Asn Gly His Thr Asp Val Thr Phe Ser Ala Gly Thr Ile Asn
165          170          175
Val Asn Asn Ser Val Glu Val Gly Asn Arg Val Gly Ser Gly Ala Gly
180          185          190
Thr His Thr Gly Thr Ala Thr Leu Asn Leu Asn Ala Asn Lys Val Thr
195          200          205
Ile Asn Ser Asn Ile Ser Ala Tyr Lys Thr Ser Gln Val Asn Val Gly
210          215          220
Asn Ala Asn Ser Val Ile Thr Ile Asn Ser Val Ser Leu Asn Gly Glu
225          230          235          240
Tyr Leu Gln Phe Phe Ser
245

```

(2) INFORMATION FOR SEQ ID NO:1690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

1229

```

Lys Ile Asp Ser Tyr Thr Ile Asn Leu Gly Arg Cys Ile Tyr Cys Gly
    115          120          125
Leu Cys Ala Glu Val Cys Pro Glu Leu Ala Ile Val Met Gly Asn Arg
    130          135          140
Phe Glu Asn Ala Ser Thr Gln Arg Ser Gln Tyr Gly Ser Lys Ser Glu
    145          150          155          160
Phe Leu Thr Ser Glu Gln Asp Ala Lys Asn Cys Ser His Ala Glu Phe
    165          170          175
Leu Gly Phe Gly Ala Val Ser Pro Asn Tyr Asn Glu Arg Met Gln Ala
    180          185          190
Thr Pro Leu Asp Tyr Val Gln Glu Pro Ser Lys Glu Glu Ser Lys Glu
    195          200          205
Glu Ser Pro Thr Ser Pro Glu Ser His Lys Gly Asp Glu Asn Val
    210          215          220

```

(2) INFORMATION FOR SEQ ID NO:1688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1688

```

Ile Met Ser Lys Asn Leu Gln Lys Lys Asn Pro Lys Lys Ser Leu Gln
1      5      10      15
Gln Ala Gln Lys Ala Ile Arg Glu Met Lys Met Phe Glu Thr Ile Ala
    20      25      30
Phe Tyr Phe Phe Ala Ile Leu Thr Leu Ser Met Ala Leu Val Val Ile
    35      40      45
Thr Thr Thr Asn Ile Leu Tyr Ala Ile Thr Ala Leu Ala Ser Ser Met
    50      55      60
Val Phe Ile Ser Ala Phe Phe Phe Leu Leu Asp Ala Glu Phe Leu Gly
    65      70      75      80
Val Val Gln Ile Thr Val Tyr Val Gly Ala Val Ile Val Met Tyr Ala
    85      90      95
Phe Gly Met Met Phe Phe Asn Ser Ala Ala Glu Val Val Glu Arg Lys
    100     105     110
Gln Ser Pro Lys Ile Leu Cys Val Leu Ser Phe Gly Val Ala Leu Leu
    115     120     125
Leu Thr Leu Ile Leu Ser Ala Pro Ser Ile Gly Glu Asn Leu Ser Lys
    130     135     140
Gln Val Asn Ser Asn Ala Ile Asp Ala Gln Ile Pro Asn Ile Lys Ala
    145     150     155     160
Ile Gly Tyr Val Leu Phe Thr Asn Tyr Leu Ile Pro Phe Glu Ala Ala
    165     170     175
Ala Leu Met Leu Leu Val Ala Met Val Gly Gly Ile Ala Thr Gly Ile
    180     185     190
Gln Lys Ile His Gly Lys Asn His Thr Gln Phe Ile Lys Glu Ser Leu
    195     200     205

```

(2) INFORMATION FOR SEQ ID NO:1689:

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```

      50              55              60
Asn Leu Glu Thr Tyr Glu Lys Ile Leu Ala Leu Leu Gln Lys Ser Asn
65              70              75              80
Asn Thr Leu Leu Val Val Gly Glu Glu Ile Tyr Ser His Lys Gln Ala
      85              90              95
His Asn Ile Ala Lys Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile
      100              105              110
Lys Leu Ile Leu Ile Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser
      115              120              125
Ile Cys Glu Leu Ser Glu Glu Val Phe Glu His Glu Lys Ile Val Gly
      130              135              140
Ile Arg Ala Gln Gly Asp Phe Thr Ile Asn Ser Asp Asp Arg Val Phe
145              150              155              160
Gly Lys Asp Ala Val Ser Lys Val Asp Phe Ile Leu Pro Ser Leu Asn
      165              170              175
Gln Leu Glu Gly Thr Ile Thr Asn Val Glu Gly Arg Val Leu Pro Leu
      180              185              190
Lys Pro Ala Leu Arg Phe Glu Gly Tyr Asp Leu Ser Asp Ile Met Gln
      195              200              205
Gly Phe Gly Phe Val Glu Glu Asn Leu Thr Glu Cys Thr His Lys Leu
      210              215              220
Pro Thr Glu Ala Gly Phe Lys Ala Leu Glu Phe Asp His Leu Thr Asn
225              230              235              240
Tyr Phe Thr Asn Asp Arg Ala Asn His Arg Gly Tyr Leu Leu Gly Thr
      245              250              255
Ser His Phe Glu Asn Ser Ala Lys Glu Ser Lys Pro Gln Asn Ala Ser
      260              265              270
Leu Ser Ser Leu
      275

```

(2) INFORMATION FOR SEQ ID NO:1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1687

```

Gly Gly Phe Met Ala Lys Gln Glu Tyr Lys Gln Leu Pro Lys Arg Ala
1              5              10              15
Glu Val His Ser Ala Thr Glu Gln Phe Lys Asp Thr Ile Lys Thr Ser
      20              25              30
Leu Gly Leu Asp Leu Phe Lys Gly Leu Gly Leu Thr Ile Lys Glu Phe
      35              40              45
Phe Ser Pro Ser Val Thr Ile His Tyr Pro Met Glu Gln Leu Pro Leu
      50              55              60
Ser Pro Arg Tyr Arg Ala Val His His Leu Gln Arg Leu Leu Asp Ser
65              70              75              80
Gly Ser Glu Arg Cys Ile Gly Cys Gly Leu Cys Glu Lys Ile Cys Thr
      85              90              95
Ser Asn Cys Ile Arg Ile Ile Thr His Lys Gly Glu Asp Asn Arg Lys
      100              105              110

```

1227

```

Ile Ser Val Phe Leu Phe Ile Gly Ala Met Gly Lys Ser Ala Gln Phe
225      230      235      240
Pro Met His Thr Trp Leu Ala Asn Ala Met Glu Gly Pro Thr Pro Val
      245      250      255
Ser Ala Leu Ile His Ala Ala Thr Met Val Thr Ala Gly Val Tyr Leu
      260      265      270
Ile Ile Arg Ala Asn Pro Leu Tyr Ser Ala Val Phe Glu Val Gly Tyr
      275      280      285
Phe Ile Ala Cys Leu Gly Ala Phe Val Ala Leu Phe Gly Ala Ser Met
      290      295      300
Ala Leu Val Asn Lys Asp Leu Lys Arg Ile Val Ala Tyr Ser Thr Leu
305      310      315      320
Ser Gln Leu Gly Tyr Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala
      325      330      335
Ile Ala Leu Phe His Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu
      340      345      350
Phe Leu Gly Ser Gly Asn Val Met His Ala Met Glu Asp Asn Leu Asp
      355      360      365
Ile Thr Lys Met Gly Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val
      370      375      380
Phe Met Ile Ile Gly Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala
385      390      395      400
Gly Tyr Phe Ser Lys Asp Lys Ile Leu Glu Val Ala Phe Gly Met His
      405      410      415
His His Ile Leu Trp Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala
      420      425      430
Phe Tyr Ser Phe Arg Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln
      435      440      445
His Glu Ile Asn His Pro His Glu Gly Gln Lys Phe His Ala Phe Glu
      450      455      460
His Ala Thr Val Arg Gly Phe Gly Gly His Cys Arg Phe Phe Arg Arg
465      470      475      480
Ala Val Phe Ser Phe Tyr Leu Ser Ser Glu Phe Leu Val Leu Glu Ser
      485      490      495
Ile

```

(2) INFORMATION FOR SEQ ID NO:1686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1686

```

Asn Lys Pro Asn Lys Gly Ala Val Leu Glu Lys Thr Lys Lys Arg Gln
1      5      10      15
Leu Leu Gln Lys Lys Thr Lys Lys Arg Ile Lys Gln Lys Arg Leu Pro
      20      25      30
Gln Lys Lys Ile Lys Gln Lys Thr Arg Gln Arg Leu Lys Arg Lys Ile
      35      40      45
Glu Val Pro Thr Lys Thr Thr Tyr Leu Leu Leu Glu Glu Ala Gly Ile

```

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(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1684

```

Lys Gly Cys Phe Met Arg Glu Phe Phe Lys Lys Leu Gly Thr Glu Tyr
1      5      10      15
Ala Ser Lys Leu Phe Leu Val Tyr Trp Leu Arg Trp Met Leu Ser Ala
      20      25      30
Leu Val Met Leu Pro Phe Met Glu Val Phe Tyr Tyr Phe Asn Phe Pro
      35      40      45
Leu Trp Leu Asn Leu Phe Leu Gly Gln Thr Ile Gly Ala Val Ile Phe
      50      55      60
Phe Lys Leu Asp Lys Leu Ile Phe Ser Lys Lys
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:1685:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 497 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1685

```

Phe Phe Lys Arg Tyr Glu Arg Leu Ser Met Gln Tyr Ser Ser Leu Leu
1      5      10      15
Ser Val Val Leu Phe Leu Pro Leu Ile Gly Ala Val Tyr Ala Gly Leu
      20      25      30
Phe Gly Ala Lys Ala Lys Ala Leu His Val Gly Val Phe Asn Ser Leu
      35      40      45
Cys Val Leu Val Ser Phe Ile Gly Ala Val Val Leu Phe Ile Gln Ala
      50      55      60
Trp His His Gln Ser Tyr Glu Lys Tyr Leu Phe Asp Trp Ile Val Val
65      70      75      80
Gly Asn Phe Lys Val Gly Phe Ser Leu Met Leu Asp Asn Ile Asn Ala
      85      90      95
Val Met Ile Val Val Val Thr Leu Val Ser Phe Leu Val His Val Tyr
      100      105      110
Ser Ile Gly Tyr Met Glu His Asp Thr Gly Phe Asn Arg Tyr Phe Ser
      115      120      125
Tyr Leu Ser Gly Phe Val Phe Ser Met Leu Val Leu Val Leu Ser Asp
      130      135      140
Asn Phe Leu Gly Leu Phe Ile Gly Trp Glu Gly Val Gly Leu Cys Ser
145      150      155      160
Tyr Leu Leu Ile Gly Phe Trp Tyr His Lys Lys Ser Ala Asn Asn Ala
      165      170      175
Ser Ile Glu Ala Phe Val Met Asn Arg Ile Thr Asp Leu Gly Met Leu
      180      185      190
Met Gly Ile Ile Leu Ile Phe Trp Asn Phe Gly Thr Leu Gln Tyr Lys
      195      200      205
Glu Val Phe Ser Met Leu Asn Asn Ala Asp Tyr Ser Met Leu Phe Tyr
210      215      220

```

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```

Leu Ala Arg Arg Val Thr Glu Ser Glu Leu Ala Gln Lys Ser Pro Phe
225                      230                      235                      240
Val Met Leu Ala Lys Glu Val Pro Asn Ala His Lys Arg Met Gly Asp
                      245                      250                      255
Tyr Gly Leu Ala Val Val Gln Gln Ser Asp Asn Ser Phe Val Leu Leu
                      260                      265                      270
Ala Thr Gln Phe Asn Pro Leu Thr Leu Asn Arg Ala Ser Ala Glu Glu
                      275                      280                      285
Ile Gln Asp His Glu Cys Ala Ile Leu Arg
290                      295

```

(2) INFORMATION FOR SEQ ID NO:1683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1683

```

Tyr His Arg Thr Asn Thr Thr Ile Arg Ile Ile Ile Met Gln Asp Leu
1                      5                      10                      15
Pro Pro Cys Pro Lys Arg Asn Asp Ala Tyr Thr Tyr His Asp Gly Thr
20                      25                      30
Gln Phe Val Cys Ser Ser Cys Leu Tyr Glu Trp Asn Gly Asn Glu Ile
35                      40                      45
Ser Asn Glu Glu Leu Ile Val Lys Asp Cys His Asn Asn Leu Leu Gln
50                      55                      60
Asn Gly Asp Ser Val Ile Leu Ile Lys Asp Leu Lys Val Lys Gly Ser
65                      70                      75                      80
Ser Leu Val Leu Lys Lys Gly Thr Lys Ile Lys Asn Ile Lys Leu Val
85                      90                      95
Asn Ser Asp His Asn Val Asp Cys Lys Val Glu Gly Gln Ser Leu Ser
100                      105                      110
Leu Lys Ser Glu Phe Leu Lys Lys Ala
115                      120

```

(2) INFORMATION FOR SEQ ID NO:1684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

1224

```

      180      185      190
Ser His Ala Ser Leu Met Thr Met Ala Ile Val Gln Gly Lys Trp Asp
      195      200      205
Leu Leu Arg Cys Cys Ser Lys Asp Arg Met His Gln Tyr Lys Arg Met
      210      215      220
Gln Thr Tyr Pro Val Leu Phe Ala Ile Gln Lys Leu Ala Leu Glu Asn
      225      230      235      240
Asn Ala Leu Met Ser Thr Leu Ser Gly Ser Gly Ser Ser Phe Phe Asn
      245      250      255
Met Cys Tyr Glu Asp Ala Pro Lys Leu Lys Gln Val Leu Ser Lys
      260      265      270
Lys Phe Pro Lys Phe Arg Val Ala Val Leu Asp Phe Asp Asn Asp Gly
      275      280      285
Val Leu Ile Glu Lys Asp
      290

```

(2) INFORMATION FOR SEQ ID NO:1682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1682

```

Leu Val Phe Lys Lys Pro Phe Phe Lys Asn Arg Leu Leu Asn Val Thr
1      5      10      15
Asn Lys Leu Lys Phe Val Lys Ile Thr Ile Met Ile Lys Asp Phe Asn
      20      25      30
His Tyr Cys Arg Lys Ile Thr Arg Gly Phe Val Lys Ile Pro Thr Lys
      35      40      45
Lys Gln Gly Ala Lys Lys Met Lys Lys Ala Gly Phe Leu Phe Leu Ala
      50      55      60
Ala Met Ala Ile Ile Val Val Ser Leu Asn Ala Lys Asp Pro Asn Val
      65      70      75      80
Leu Arg Lys Ile Val Phe Glu Lys Cys Leu Pro Asn Tyr Glu Lys Asn
      85      90      95
Gln Asn Pro Ser Pro Cys Ile Glu Val Lys Pro Asp Ala Gly Tyr Val
      100      105      110
Val Leu Lys Asp Ile Asn Gly Pro Leu Gln Tyr Leu Leu Met Pro Thr
      115      120      125
Thr His Ile Ser Gly Ile Glu Asn Pro Leu Leu Leu Asp Pro Ser Thr
      130      135      140
Pro Asn Phe Phe Tyr Leu Ser Trp Gln Ala Arg Asp Phe Met Ser Lys
      145      150      155      160
Lys Tyr Gly Lys Pro Ile Pro Asp Tyr Ala Ile Ser Leu Thr Ile Asn
      165      170      175
Ser Lys Lys Gly Arg Ser Gln Asn His Phe His Ile His Ile Ser Cys
      180      185      190
Ile Ser Leu Asp Val Arg Lys Gln Leu Asp Asn Asn Leu Lys Asn Ile
      195      200      205
Asn Ser Arg Trp Ser Pro Leu Ser Gly Gly Leu Asn Gly His Lys Tyr
      210      215      220

```

1223

Gly Val Tyr Asp Lys Ser Leu Cys Lys Thr Met Ala Leu Ala Leu Lys
 85 90 95
 Ala Leu Gly Val Lys Arg Ala Met Val Val Asn Gly Gly Gly Thr Asp
 100 105 110
 Glu Ile Val Leu His Asp Ile Thr His Ala Cys Glu Leu Lys Asn Asn
 115 120 125
 Glu Ile Leu Glu Tyr Asp Leu Ser Ala Lys Asp Phe Asp Leu Pro Pro
 130 135 140
 Tyr Asp Leu Lys Glu Leu Gln Ile Glu Asn Ala Lys Glu Ser Val Gln
 145 150 155 160
 Ala Cys Leu Asp Ile Leu Glu Asn Lys Gly Lys Asp Ser His Thr Met
 165 170 175
 Val Val Ala Ala Asn Val Ala Ser Leu Leu Tyr Leu Ser His Arg Ala
 180 185 190
 Lys Gly Phe Lys Arg Gly Arg Glu His Asp Phe Arg Ala Phe Lys Asn
 195 200 205
 Gln Ser Ala Leu Cys Ala Phe Thr Lys Asn His Lys Ala Lys Pro Cys
 210 215 220
 Leu Ala Cys
 225

(2) INFORMATION FOR SEQ ID NO:1681:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1681

Asn Leu Val Val Ser Val Pro Ala Thr Ser Ala Asn Leu Gly Pro Gly
 1 5 10 15
 Phe Asp Cys Leu Gly Leu Ser Leu Asn Leu Arg Asn Arg Phe Phe Ile
 20 25 30
 Glu Pro Ser Asn Ile His Ala Val Lys Leu Val Gly Glu Gly Glu Gly
 35 40 45
 Ile Pro Lys Phe Leu Thr Asn Asn Ile Phe Thr Lys Val Phe Tyr Glu
 50 55 60
 Ile Leu Lys Lys His Gly Asn Asp Gly Ser Phe Lys Phe Leu Leu His
 65 70 75 80
 Asn Lys Val Pro Ile Thr Arg Gly Met Gly Ser Ser Ser Ala Met Ile
 85 90 95
 Val Gly Ala Val Ala Ser Ala Phe Ala Phe Leu Gly Phe Ala Phe Asp
 100 105 110
 Arg Glu Asn Ile Leu Asn Thr Ala Leu Ile Tyr Glu Asn His Pro Asp
 115 120 125
 Asn Ile Thr Pro Ala Val Phe Gly Gly Tyr Asn Ala Ala Phe Val Glu
 130 135 140
 Lys Lys Lys Val Ile Ser Leu Lys Thr Lys Ile Pro Ser Phe Leu Lys
 145 150 155 160
 Ala Val Met Val Ile Pro Asn Arg Val Ile Ser Thr Lys Gln Ser Arg
 165 170 175
 His Leu Leu Pro Lys Arg Tyr Ser Val Gln Glu Ser Val Phe Asn Leu

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```

145          150          155          160
Thr Asn Ala Leu Glu Lys Thr Leu Ser Val Phe Thr Pro Ile Asp Tyr
165          170          175
Asp His Lys Glu Phe Leu Gly Asp Ser Leu Glu Ser Ile Ala Thr Thr
180          185          190
Lys Leu Lys Ala Met Gly Ser Leu Asn Ile Ile Ala Pro Gln Gln Glu
195          200          205
Leu Val Leu Asn Val Ala Gln Lys Ile Ala Lys Asp Lys His Ala Gln
210          215          220
Leu Ile Val Val Gln Asn Glu Ile Ser Lys Gly Val Ser Asp Tyr Ile
225          230          235          240
Glu Arg His His Leu Ala His Phe Leu Ala Met Asn Leu Glu Val Ala
245          250          255
Leu Lys Ala Phe Glu Thr Leu Leu Pro Cys Asn Lys Gln Glu Val Leu
260          265          270
Lys Asn Leu Lys Pro Leu Asp Leu Ile Gly Arg Cys Glu Leu Leu Ser
275          280          285
Pro Asn Ile Leu Ile Asp Val Gly His Asn Pro His Ser Ala Lys Ala
290          295          300
Leu Lys Glu Glu Ile Lys Arg Ile Phe Asn Ala Pro Ile Val Leu Ile
305          310          315          320
Tyr Asn Cys Tyr Gln Asp Lys Asp Ala Phe Leu Val Leu Glu Ile Leu
325          330          335
Lys Ser Val Val Lys Lys Val Leu Ile Leu Glu Leu His Asn Glu Arg
340          345          350
Ile Ile Gln Leu Glu Lys Leu Lys Gly Ile Leu Glu Thr Leu Gly Leu
355          360          365
Glu His Ala Leu Phe Glu Glu Leu Lys Glu Asn Glu Asn Tyr Leu Val
370          375          380
Tyr Gly Ser Phe Leu Val Ala Asn Ala Phe Tyr Glu Arg Tyr Pro Lys
385          390          395          400
Lys Arg Asp

```

(2) INFORMATION FOR SEQ ID NO:1680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1680

```

Ser Val Ser Ser His Ser Gly Ser Ala Asp Leu Leu Glu Asn Leu Gly
1          5          10          15
Val Asn Ile Glu Met Asn Pro Met Gln Leu Glu Asn Cys Phe Lys Gln
20          25          30
Ser His Phe Gly Phe Leu Phe Ala Pro Leu Tyr His Gln Ser Phe Lys
35          40          45
Lys Ser Ala Pro Leu Arg Lys Glu Leu Phe Thr Lys Thr Ile Phe Asn
50          55          60
Cys Leu Gly Pro Leu Ile Asn Pro Leu Arg Pro Lys Ile Gln Leu Leu
65          70          75          80

```

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Ala His Arg Phe Ile Lys Arg Leu Tyr Asp Lys Ala Asn Ala Ile Thr
 275 280 285
 Pro Thr Thr Ser Lys Pro Glu Phe Lys Glu Val Gly Leu Asn Glu Ala
 290 295 300
 Gln Lys Leu Ala Arg Lys Lys Val Tyr Glu Ala Leu Lys Lys Ser His
 305 310 315 320
 Glu Ile Phe Asn Lys Ala Glu Ser Ala Tyr Ala Phe Asn Thr Leu Ile
 325 330 335
 Ala Ser Cys Met Glu Ala Leu Asn Ala Leu Asn Ala Gln Ser Asp Glu
 340 345 350
 Gln Ile Leu Cys Glu Gly Tyr Phe Val Leu Leu Gln Ile Leu Glu Pro
 355 360 365
 Met Ile Pro His Thr Ala Trp Glu Leu Ser Glu Arg Leu Phe Lys Arg
 370 375 380
 Glu Asn Phe Lys Pro Ile Glu Val Asp Glu Ser Ala Leu Ile Glu Asp
 385 390 395 400
 Phe Met Thr Leu Gly Leu Thr Ile Asn Gly Lys Arg Arg Ala Glu Leu
 405 410 415
 Lys Val Asn Ile Asn Ala Ser Lys Glu Glu Ile Ile Ile Leu Ala Lys
 420 425 430
 Lys Glu Leu Glu Lys Tyr Leu Glu Asn Ala Ser Val Lys Lys Glu Ile
 435 440 445
 Tyr Val Pro Asn Lys Leu Val Asn Phe Val Thr Ala
 450 455 460

(2) INFORMATION FOR SEQ ID NO:1679:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1679

Leu Asn Leu Trp Leu Lys Ser Leu Met Arg Gly Asn Ser Ile Met Lys
 1 5 10 15
 Asn Ser His Gly Leu Lys Ala Phe Leu Glu Thr Lys Pro Lys Glu Tyr
 20 25 30
 His Lys Phe Asp Pro Ser Arg Phe Ile Gln Ile Tyr Lys Asp Phe Lys
 35 40 45
 Asn Ala Phe Phe Glu Ile Gln Ala Lys Val Ile His Val Val Gly Thr
 50 55 60
 Asn Gly Lys Gly Ser Thr Gly Arg Phe Leu Thr Leu Leu Leu Ala Asp
 65 70 75 80
 Gln Gly Phe Lys Val Leu His Phe Thr Ser Pro His Val Phe Glu Phe
 85 90 95
 Arg Glu Arg Phe Tyr Leu Asn Gly Ser Val Val Lys Glu Ser Val Leu
 100 105 110
 Glu Asn Ala His Gln Gln Leu Gln Ser His Ala Phe Ser Asn Ala Cys
 115 120 125
 Ser Tyr Phe Glu Tyr Ala Thr Leu Leu Ala Val Met Leu Ala Lys Asp
 130 135 140
 Cys Asp Tyr Leu Val Leu Glu Ala Gly Leu Gly Gly Glu Phe Asp Ser

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				245					250					255	
Glu	Val	Arg	Phe	Leu	Asp	Gln	Pro	Ile	Asn	Pro	Met	Ser	Phe	Thr	Lys
			260						265					270	
Trp	Asn	Met	Lys	Asp	Phe	Glu	Glu	Val	Phe	Asn	Lys	Glu	Arg	Ser	Ile
		275					280						285		
Arg	Trp	Gln	Ser	Leu	Ile	Thr	Ile	Ile	Asn	Arg	Leu	Met	Gln	Lys	Gln
	290				295						300				
Asp	Gln	Arg	Leu	Ser	Ser	Leu	Lys	Ala	Pro	Lys					
305					310					315					

(2) INFORMATION FOR SEQ ID NO:1678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...460

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1678

Asp	Ile	Glu	Phe	Ala	Asn	Leu	Tyr	His	Ile	Pro	Ile	Lys	Val	Ile	Thr
1			5						10					15	
Gln	Ser	Pro	Gln	Asn	Leu	Pro	His	Thr	Lys	Glu	Glu	Ile	Leu	Lys	Asn
			20					25					30		
Ser	Gly	Glu	Trp	Ser	Asp	Leu	Ser	Ser	Ser	Leu	Ala	Arg	Lys	Lys	Ile
		35				40					45				
Leu	Pro	Tyr	Phe	Asp	Lys	Glu	Asn	Leu	Gly	Lys	Arg	Val	Ile	Asn	Tyr
	50				55					60					
Arg	Leu	Gln	Asn	Trp	Gly	Val	Ser	Arg	Gln	Arg	Tyr	Trp	Gly	Ala	Pro
65				70					75					80	
Ile	Pro	Met	Ile	His	Cys	Lys	His	Cys	Gly	Ile	Val	Pro	Glu	Thr	Gln
			85						90				95		
Leu	Pro	Val	Thr	Leu	Pro	Glu	Asp	Ile	Val	Ile	Asp	Gly	Glu	Gly	Asn
		100					105					110			
Pro	Leu	Lys	Lys	His	Ala	Ser	Trp	Arg	Phe	Ala	Gln	Cys	Pro	Arg	Cys
		115				120					125				
His	Lys	Asp	Ala	Leu	Val	Glu	Thr	Asp	Thr	Met	Asp	Thr	Phe	Ile	Gln
	130				135					140					
Ser	Ser	Trp	Tyr	Phe	Leu	Arg	Tyr	Thr	Thr	Pro	Lys	Asn	Gln	Arg	Glu
145				150					155					160	
Asn	Gln	Ala	Phe	Asp	Gln	Asn	Tyr	Leu	Lys	Tyr	Phe	Met	Pro	Val	Asp
			165					170					175		
Thr	Tyr	Ile	Gly	Gly	Ile	Glu	His	Ala	Ile	Leu	His	Leu	Leu	Tyr	Ala
		180					185					190			
Arg	Phe	Phe	Thr	Lys	Ala	Leu	Arg	Asp	Leu	Gly	Tyr	Leu	His	Leu	Asp
	195					200					205				
Glu	Pro	Phe	Lys	Gln	Leu	Ile	Thr	Gln	Gly	Met	Val	Leu	Lys	Asp	Gly
	210				215						220				
Ala	Lys	Met	Ser	Lys	Ser	Lys	Gly	Asn	Val	Val	Ser	Pro	Lys	Glu	Ile
225				230					235					240	
Leu	Lys	Lys	Tyr	Gly	Ala	Asp	Ala	Val	Arg	Leu	Phe	Ile	Leu	Phe	Ala
			245					250					255		
Ala	Pro	Pro	Ala	Lys	Glu	Leu	Glu	Trp	Asn	Asp	Asn	Ala	Leu	Glu	Gly
		260					265						270		

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```

Asp His Val Asn Val Gln Pro Lys Ser Phe Ile Gln Lys Gly Gln Leu
225                230                235                240
Ile Gly Tyr Ser Gly Lys Ser Gly Asn Ser Gly Gly Glu Lys Leu His
                245                250                255
Tyr Glu Val Arg Phe Leu Gly Lys Ile Leu Asp Ala Glu Lys Phe Leu
                260                265                270
Ala Trp Asp Leu Asp His Phe Gln Ser Ala Leu Glu Glu Asn Lys Phe
                275                280                285
Ile Glu Trp Lys Asn Leu Phe Trp Val Leu Glu Asp Ile Val Gln Leu
                290                295                300
Gln Glu His Val Asp Lys Asp Thr Leu Lys Gly Gln
305                310                315

```

(2) INFORMATION FOR SEQ ID NO:1677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1677

```

Gly Phe Leu Val Phe Leu Asp Arg Arg Leu Ile Val Met Val Thr Asp
1          5          10          15
Ser Lys Gly Ser Arg Tyr Ile Asn Val His Ile Leu Phe Arg Gln Ile
          20          25          30
Ser Leu Tyr Ala Leu Leu Ser Val Val Gly Ser Leu Leu Phe Leu Gly
          35          40          45
Val Ser Leu Leu Val Leu Asn Lys Glu Ile Lys Asn Ile Glu Lys Gln
          50          55          60
His Ala Leu Ile Thr Lys Glu Phe Glu Lys Lys Arg Glu Thr Asn Glu
65          70          75          80
Lys Leu Ser Leu Gln Met Asp Glu Phe Leu Asp Asp Leu Gln Leu Ser
          85          90          95
Gly Glu Arg Ile Asn Asp Leu Glu Glu Val Val Gly Val Asn Arg Pro
          100         105         110
Glu Glu Glu Lys Glu Glu Gly Asn Phe Ser Ser Arg Leu Asp Val Ala
          115         120         125
Gly Ile Thr Gly Leu Gln Lys Ser Phe Ile Met Arg Leu Ile Pro Asn
130         135         140
Asp Tyr Pro Leu Glu Ser Tyr Arg Arg Val Ser Ala Ala Phe Asn Lys
145         150         155         160
Arg Met His Pro Ile Leu His Val Leu His Asn His Thr Gly Leu Asp
          165         170         175
Leu Ser Thr Ala Ile Asn Thr Pro Val Tyr Ala Ser Ala Ser Gly Val
          180         185         190
Val Gly Leu Ala Ser Lys Gly Trp Asn Gly Gly Tyr Gly Asn Leu Ile
          195         200         205
Lys Val Phe His Pro Phe Gly Phe Lys Thr Tyr Tyr Ala His Leu Asn
210         215         220
Lys Ile Val Val Lys Thr Gly Glu Phe Val Lys Lys Gly Gln Leu Ile
225         230         235         240
Gly Tyr Ser Gly Asn Thr Gly Met Ser Thr Gly Pro His Leu His Tyr

```

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```

305          310          315          320
Gln Ala Gly Ile Ala Gly Glu Ile Ile Gly Ile Lys Ile Ala Leu Asn
          325          330          335
Glu Phe Val Gly Tyr Met Gln Leu Leu Pro Tyr Leu Gly Asp Asn Pro
          340          345          350
Pro Leu Ile Leu Ser Glu Lys Thr Lys Ala Ile Ile Thr Phe Ala Leu
          355          360          365
Cys Gly Phe Ala Asn Leu Ser Ser Val Ala Met Leu Ile Gly Gly Leu
          370          375          380
Gly Ser Leu Val Pro Lys Lys Asp Phe Ile Ala Arg Leu Ala Leu
385          390          395          400
Lys Ala Val Leu Val Gly Thr Leu Ser Asn Phe Met Ser Ala Thr Ile
          405          410          415
Ala Gly Leu Phe Ile Gly Leu Ser Ala Asn
          420          425

```

(2) INFORMATION FOR SEQ ID NO:1676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...316

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1676

```

Thr Leu Ser Lys Glu Glu Gly Leu Met Pro Gln Asn Gln Leu Val Ile
1          5          10          15
Thr Ile Ile Asp Glu Ser Gly Ser Lys Gln Leu Lys Phe Ser Lys Asn
          20          25          30
Leu Lys Arg Asn Leu Ile Ile Ser Val Val Ile Leu Leu Leu Ile Val
          35          40          45
Gly Leu Gly Val Gly Phe Leu Lys Phe Leu Ile Ala Lys Met Asp Thr
50          55          60
Met Thr Ser Glu Arg Asn Ala Val Leu Arg Asp Phe Arg Gly Leu Tyr
65          70          75          80
Gln Lys Asn Tyr Ala Leu Ala Lys Glu Ile Lys Asn Lys Arg Glu Glu
          85          90          95
Leu Phe Ile Val Gly Gln Lys Ile Arg Gly Leu Glu Ser Leu Ile Glu
          100          105          110
Ile Lys Lys Gly Ala Asn Gly Gly Gly His Leu Tyr Asp Glu Val Asp
          115          120          125
Leu Glu Asn Leu Ser Leu Asn Gln Lys His Leu Ala Leu Met Leu Ile
130          135          140
Pro Asn Gly Met Pro Leu Lys Thr Tyr Ser Ala Ile Lys Pro Thr Lys
145          150          155          160
Glu Arg Asn His Pro Ile Lys Lys Ile Lys Gly Val Glu Ser Gly Ile
          165          170          175
Asp Phe Ile Ala Pro Leu Asn Thr Pro Val Tyr Ala Ser Ala Asp Gly
          180          185          190
Ile Val Asp Phe Val Lys Thr Arg Ser Asn Ala Gly Tyr Gly Asn Leu
          195          200          205
Val Arg Ile Glu His Ala Phe Gly Phe Ser Ser Ile Tyr Thr His Leu
210          215          220

```

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Phe Thr Thr Leu Phe Ala Ile Ser Gln Gly Ile Gln Pro Ile Ala Glu
 145 150 155 160
 Leu

(2) INFORMATION FOR SEQ ID NO:1675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1675

Phe Leu Asn Ile Arg Asp Leu Thr Met Ile Phe Ser Ser Leu Phe Ser
 1 5 10 15
 Val Val Gly Met Ala Val Leu Phe Leu Ile Ala Trp Val Phe Ser Gly
 20 25 30
 Asn Lys Arg Ala Ile Asn Tyr Arg Thr Ile Val Ser Ala Phe Val Ile
 35 40 45
 Gln Val Ala Leu Gly Ala Leu Ala Leu Tyr Val Pro Leu Gly Arg Glu
 50 55 60
 Ile Leu Gln Gly Leu Ala Ser Gly Ile Gln Ser Val Ile Gly Tyr Gly
 65 70 75 80
 Tyr Glu Gly Val Arg Phe Leu Phe Gly Asn Leu Ala Pro Asn Ala Lys
 85 90 95
 Gly Asp Gln Gly Ile Gly Gly Phe Ile Phe Ala Ile Asn Val Leu Ala
 100 105 110
 Ile Ile Ile Phe Phe Ala Ser Leu Ile Ser Leu Leu Tyr Tyr Leu Lys
 115 120 125
 Ile Met Pro Leu Val Ile Asn Leu Ile Gly Gly Ala Leu Gln Lys Cys
 130 135 140
 Leu Gly Thr Ser Lys Ala Glu Ser Met Ser Ala Ala Ala Asn Ile Phe
 145 150 155 160
 Val Ala His Thr Glu Ala Pro Leu Val Ile Lys Pro Tyr Leu Lys Ser
 165 170 175
 Met Ser Asp Ser Glu Ile Phe Ala Val Met Cys Val Gly Met Ala Ser
 180 185 190
 Val Ala Gly Pro Val Leu Ala Gly Tyr Ala Ser Met Gly Ile Pro Leu
 195 200 205
 Pro Tyr Leu Ile Ala Ala Ser Phe Met Ser Ala Pro Gly Gly Leu Leu
 210 215 220
 Phe Ala Lys Ile Ile Tyr Pro Gln Asn Glu Thr Ile Ser Ser His Ala
 225 230 235 240
 Asp Val Ser Ala Glu Glu His Val Asn Ile Ile Glu Ala Ile Ala Asn
 245 250 255
 Gly Ala Ser Thr Gly Leu His Leu Ala Leu His Val Gly Ala Met Leu
 260 265 270
 Leu Ala Phe Val Gly Met Leu Ala Leu Val Asn Gly Leu Leu Gly Val
 275 280 285
 Val Gly Gly Phe Leu Gly Met Glu His Leu Ser Leu Gly Val Val Leu
 290 295 300
 Gly Thr Leu Leu Lys Pro Leu Ala Phe Met Leu Gly Val Pro Trp Ser

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...130

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1673

```

Met Leu Lys Lys Lys Ile Asp Leu His Lys Asp Ser Ile Arg Lys Leu
1      5      10      15
Phe Phe Tyr Tyr Phe Ile Pro Leu Val Phe Ser Met Ile Ser Leu Ser
20      25      30
Thr Tyr Ser Met Val Asp Asp Met Phe Val Gly Lys Lys Leu Gly Lys
35      40      45
Glu Ala Ile Ala Ala Val Asn Ile Ala Trp Pro Ile Phe Pro Gly Leu
50      55      60
Ile Ala Tyr Glu Leu Leu Phe Gly Phe Gly Ala Ala Ser Ile Val Gly
65      70      75      80
Tyr Phe Leu Gly Gln Asn Lys Thr His Arg Ala Arg Leu Val Phe Ser
85      90      95
Ser Val Phe Tyr Phe Val Ala Leu Ser Ala Phe Ile Leu Ser Met Ala
100     105     110
Leu Leu Pro Phe Ser Glu Asn Ile Ala Arg Phe Leu Gly Ala Met Thr
115     120     125
Leu Tyr
130

```

(2) INFORMATION FOR SEQ ID NO:1674:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...161

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1674

```

Asn His Phe Asn Gly Cys Val Phe Arg Val Gln His Leu Leu Ala Asp
1      5      10      15
Val Phe Val Val Asn Asp Lys Arg Pro Val Leu Ala Met Val Ala Met
20      25      30
Leu Ile Gly Ser Leu Ala Asn Ile Phe Phe Asn Tyr Leu Phe Ile Phe
35      40      45
Val Leu Glu Val Gly Val Gln Gly Ser Ala Ile Ala Thr Val Ile Gly
50      55      60
His Ala Ile Gly Val Leu Val Leu Met Gln His Phe Trp Arg Lys Lys
65      70      75      80
Gly Gln Leu Tyr Phe Ile Lys Arg Phe Ser Leu Ser Ser Val Ile Ser
85      90      95
Ser Ala Lys Ser Gly Val Pro Gln Ser Thr Ala Glu Phe Ser Ala Ser
100     105     110
Ile Met Ile Leu Leu Phe Asn Thr Ala Ile Met His Thr Ala Gly Glu
115     120     125
Arg Phe Val Ser Met Tyr Gly Ile Val Met Tyr Asn Ala Ile Ile Phe
130     135     140

```

1215

```

Leu Ile Gly Ile Thr Ser Ala Leu Asn Asn Arg Gly Asn Lys Glu Glu
 290                      295                      300
Val Thr Asn Phe Phe Gly Asp Tyr Leu Leu Leu Gln Leu Met Arg Gln
305                      310                      315                      320
Ser Gly Met Gly Ile Asn Gln Val Val Asn Gln Ile Leu Arg Asp Lys
                      325                      330                      335
Ser Lys Ile Ala Pro Ile Val Val Ile Arg Glu Gly Ser Arg Val Phe
                      340                      345                      350
Ile Ser Pro Asn Thr Asp Ile Phe Phe Pro Ile Pro Arg Glu Asn Glu
                      355                      360                      365
Val Ile Ala Glu Phe Leu Lys
 370                      375

```

(2) INFORMATION FOR SEQ ID NO:1672:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1672

```

Lys Ala Ala Phe Cys Ile Gly Ile Phe Phe Tyr Gly Ala Tyr Tyr Phe
 1                      5                      10                      15
Leu Asp Glu Phe Leu Ile Lys Leu Tyr Leu Gln Pro Ser Glu Gln Asp
                      20                      25                      30
Ala Leu Phe Met Gln Glu Thr Lys Arg Ala Met Asn Ile Tyr Tyr Val
                      35                      40                      45
Gly Tyr Val Phe Leu Gly Met Thr Leu Leu Cys Ala Val Phe Phe Gln
                      50                      55                      60
Ser Ile Gln Arg Thr Lys Ser Ser Phe Ile Ile Thr Ile Ser His Thr
                      65                      70                      75                      80
Leu Gly Phe Ile Val Ile Leu Leu Pro Ile Leu Ser His Phe Tyr Gly
                      85                      90                      95
Val Asn Gly Ile Trp Val Thr Tyr Pro Ile Ala Gln Phe Leu Ala Val
                      100                      105                      110
Phe Gly Ser Val Arg Gly Asn Leu Leu
 115                      120

```

(2) INFORMATION FOR SEQ ID NO:1673:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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```

385          390          395          400
Leu Asp Ile Tyr Glu Ile Val Pro Gly Phe Ile Val Ala Ser Val Ala
          405          410          415
Ile Val Ala Phe Ser Leu Phe Ser Ser Val Arg Ser Gly Thr Lys Glu
          420          425          430
Ala Phe Glu Thr Met Leu Lys Glu Ile Glu Ser Leu Lys His
          435          440          445

```

(2) INFORMATION FOR SEQ ID NO:1671:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1671

```

Asn Lys Trp Ile Lys Gly Ala Val Val Phe Val Gly Gly Phe Ala Thr
1          5          10          15
Ile Thr Thr Phe Ser Leu Ile Tyr His Gln Lys Pro Lys Ala Pro Leu
          20          25          30
Asn Asn Gln Pro Ser Leu Leu Asn Asp Asp Glu Val Lys Tyr Pro Leu
          35          40          45
Gln Asp Tyr Thr Phe Thr Gln Asn Pro Gln Pro Thr Asn Thr Glu Ser
          50          55          60
Ser Lys Asp Ala Thr Ile Lys Ala Leu Gln Glu Gln Leu Lys Ala Ala
          65          70          75          80
Leu Lys Ala Leu Asn Ser Lys Glu Met Asn Tyr Ser Lys Glu Glu Thr
          85          90          95
Phe Thr Ser Pro Pro Met Asp Pro Lys Thr Thr Pro Pro Lys Lys Asp
          100          105          110
Phe Ser Pro Lys Gln Leu Asp Leu Leu Ala Ser Arg Ile Thr Pro Phe
          115          120          125
Lys Gln Ser Pro Lys Asn Tyr Glu Glu Asn Leu Ile Phe Pro Val Asp
          130          135          140
Asn Pro Asn Gly Ile Asp Ser Phe Thr Asn Leu Lys Glu Lys Asp Ile
          145          150          155          160
Ala Thr Asn Glu Asn Lys Leu Leu Arg Thr Ile Thr Ala Asp Lys Met
          165          170          175
Ile Pro Ala Phe Leu Ile Thr Pro Ile Ser Ser Gln Ile Ala Gly Lys
          180          185          190
Val Ile Ala Gln Val Glu Ser Asp Ile Phe Ala Ser Met Gly Lys Ala
          195          200          205
Val Leu Ile Pro Lys Gly Ser Lys Val Ile Gly Tyr Ser Asn Asn
          210          215          220
Asn Lys Met Gly Glu Tyr Arg Leu Asp Ile Val Trp Ser Arg Ile Ile
          225          230          235          240
Thr Pro His Gly Ile Asn Ile Met Leu Thr Asn Ala Lys Gly Ala Asp
          245          250          255
Ile Lys Gly Tyr Asn Gly Leu Val Gly Glu Leu Ile Glu Arg Asn Phe
          260          265          270
Gln Arg Tyr Gly Val Pro Leu Leu Leu Ser Thr Leu Thr Asn Gly Leu
          275          280          285

```

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1670

```

Arg Phe Glu Cys Gly Ala Ser Asp Met Ser Gly Trp Leu Leu Met Gly
1      5      10      15
Leu Pro Gly Ala Leu Tyr Val Gly Gly Leu Ile Asn Ser His Ile Ala
20      25      30
Ile Gly Leu Ser Leu Gly Ala Leu Ile Asn Trp Val Phe Val Ala Lys
35      40      45
Arg Leu Arg Ile Tyr Thr Ser Val Ile Ala Asn Ser Ile Thr Ile Ser
50      55      60
Asp Tyr Phe Glu Thr Arg Phe Ser Asp Asp Lys His Ile Leu Arg Leu
65      70      75      80
Ile Ser Ala Phe Val Ile Leu Ile Leu Lys Ile Phe Tyr Phe Ser Ser
85      90      95
Gly Leu Val Ser Gly Ala Lys Leu Phe Glu Pro Thr Phe Gly Ile Gln
100     105     110
Tyr Thr Tyr Ala Leu Ser Ile Gly Thr Leu Ile Ile Val Ser Tyr Thr
115     120     125
Phe Leu Gly Arg Tyr Lys Ala Val Cys Trp Thr Asp Leu Ile Gln Gly
130     135     140
Leu Leu Met Met Ser Ala Leu Ile Val Val Pro Ile Val Met Ile Ile
145     150     155     160
His Leu Gly Gly Ile Gly Glu Gly Ile Lys Ile Ile Lys Glu Ile Lys
165     170     175
Pro Glu Asn Leu Ser Phe Leu Gln Gly Ser Ser Val Val Ala Ile Ile
180     185     190
Ser Ser Leu Ala Trp Gly Leu Gly Tyr Phe Gly Gln Pro His Ile Leu
195     200     205
Val Arg Phe Met Ser Ile Arg Ser Ile Arg Asp Val Pro Lys Ala Thr
210     215     220
Thr Ile Gly Ile Ser Trp Met Val Ile Ser Leu Ile Gly Ala Cys Val
225     230     235     240
Met Gly Leu Leu Gly Val Ala Tyr Val His Lys Phe Asp Leu Ser Leu
245     250     255
Glu Asp Pro Glu Lys Ile Phe Ile Val Met Ser Gln Leu Leu Phe Asn
260     265     270
Pro Trp Ile Thr Gly Ile Leu Leu Ser Ala Ile Leu Ala Ala Val Met
275     280     285
Ser Thr Ala Ser Ser Gln Leu Leu Val Ser Ser Ser Thr Ile Ala Glu
290     295     300
Asp Phe Tyr Ala Thr Ile Phe Asn Lys Asn Ala Pro Gln Lys Leu Val
305     310     315     320
Met Thr Ile Ser Arg Leu Ser Val Leu Gly Val Ala Cys Ile Ala Phe
325     330     335
Phe Ile Ser Thr Asp Lys Asn Ala Ser Ile Leu Ser Ile Val Ser Tyr
340     345     350
Ala Trp Ala Gly Phe Gly Ala Ser Phe Gly Ser Val Ile Leu Phe Ser
355     360     365
Leu Phe Trp Ser Arg Met Thr Arg Ile Gly Ala Ile Ala Gly Met Leu
370     375     380
Ser Gly Ala Ser Thr Val Ile Leu Tyr Asp Lys Phe Gly Lys Ser Phe

```


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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1669

```

Ala His Ala Asn Arg Thr Ile Ile His Arg Ile Asp Asp Ser Ile Ala
1      5      10      15
Gln Arg Val Asp Asn Ala Ile Arg Pro Met Arg Leu Val Arg Gly Phe
20     25     30
Ala Pro Leu Tyr Leu Thr Leu Pro Lys Arg Ser Phe Asn Ala Pro Lys
35     40     45
Lys Ile Leu Ala Leu Gly Ala Glu Gln Lys Gly His Phe Ser Leu Leu
50     55     60
Asp Ser Glu Thr Ser Val Leu Leu Ser Pro Phe Cys Gly Asp Leu
65     70     75     80
Ser Val Leu Glu Asn Glu Lys His Phe Lys Glu Thr Leu Asn Phe Phe
85     90     95
Leu Lys Thr Tyr Asp Phe Lys Pro Thr Leu Leu Ala Cys Asp Glu His
100    105    110
Gln Asn Tyr Thr Thr Thr Lys Met Ala Phe Asp Phe Asn Thr Pro Leu
115    120    125
Leu Gln Val Gln His His His Ala His Phe Leu Ala Ser Val Leu Asp
130    135    140
Ala Leu Leu Gln Asp Pro His Leu Asn His Pro Phe Ile Gly Ile Val
145    150    155    160
Trp Asp Gly Ser Gly Ala Tyr Glu Asn Lys Ile Tyr Gly Ala Glu Cys
165    170    175
Phe Val Gly Asp Leu Glu Arg Ile Glu Glu Val Ala Arg Phe Glu Glu
180    185    190
Phe Trp Leu Leu Gly Gly Gln Lys Ala Ile Lys Glu Pro Arg Arg Leu
195    200    205
Val Leu Glu Ile Ala Leu Lys His Gln Leu Asn Lys Leu Leu Lys Arg
210    215    220
Val Gln Lys His Phe Lys Glu Asp Glu Leu Gly Ile Phe Lys Gln Met
225    230    235    240
His Asp Lys Lys Ile Gln Ser Val Ala Thr Asn Ser Ile Gly Arg Leu
245    250    255
Phe Asp Ile Val Ala Phe Ser Leu Gly Val Val Gly Thr Ile Ser Phe
260    265    270
Glu Ala Glu Ser Gly Gln Val Leu Glu Asn Leu Ala Leu Gln Ser Asp
275    280    285
Glu Ile Ala Phe Tyr Pro Phe Glu Ile Lys Asn Ser Val Val Arg Leu
290    295    300
Lys Glu Phe Tyr Gln Ala Phe Glu Lys Asp Leu Gly Val Leu Glu Pro
305    310    315    320
Lys Arg Ile Ala Lys Lys Phe Phe Asn Ser Leu Val Glu Ile Ile Thr
325    330    335
Ala Leu Ile Ala Pro Phe Lys Gly His Val Val Val Cys Ser Gly Gly
340    345    350
Val Phe Cys Asn Gln Leu Leu Cys Glu Gln Leu Ala Lys Arg Leu Lys
355    360    365
Lys Leu Gln Arg Glu Tyr Phe Phe His Lys His Phe Pro Pro Asn Asp
370    375    380
Ser Ser Ile Pro Val Gly Gln Ala Leu Met Ala Tyr Phe Asn Pro Thr
385    390    395    400
Ile Ile Lys Lys Gly
405

```

(2) INFORMATION FOR SEQ ID NO:1670:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids

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(2) INFORMATION FOR SEQ ID NO:1668:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1668

```

Gly Ile Phe Met Asn Glu Ile Ile Leu Ile Thr Gly Ala Tyr Gly Met
1      5      10      15
Val Gly Gln Asn Thr Ala Leu Tyr Phe Lys Lys Asn Lys Pro Asp Val
      20      25      30
Thr Leu Leu Thr Pro Lys Lys Ser Glu Leu Tyr Leu Leu Asp Lys Asp
      35      40      45
Asn Val Gln Ala Tyr Leu Lys Glu Tyr Lys Pro Thr Gly Ile Ile His
      50      55      60
Cys Ala Gly Arg Val Gly Gly Ile Val Ala Asn Met Asn Asp Leu Ser
      65      70      75      80
Thr Tyr Met Val Glu Asn Leu Leu Met Gly Leu Tyr Leu Phe Ser Ser
      85      90      95
Ala Leu Asp Leu Gly Val Lys Lys Ala Ile Asn Leu Ala Ser Ser Cys
      100     105     110
Ala Tyr Pro Lys Tyr Ala Pro Asn Pro Leu Lys Glu Ser Asp Leu Leu
      115     120     125
Asn Gly Ser Leu Glu Pro Thr Asn Glu Gly Tyr Ala Leu Ala Lys Leu
      130     135     140
Ser Val Met Lys Tyr Cys Glu Tyr Val Ser Ala Glu Lys Gly Val Phe
      145     150     155     160
Tyr Lys Thr Leu Val Pro Cys Asn Leu Tyr Gly Glu Phe Asp Lys Phe
      165     170     175
Glu Glu Lys Ile Ala His Met Ile Pro Gly Leu Ile Ala Arg Met His
      180     185     190
Thr Ala Lys Leu Lys Asn Glu Lys Asn Phe Ala Met Trp Gly Asp Gly
      195     200     205
Thr Ala Glu Glu Ser Ile
      210

```

(2) INFORMATION FOR SEQ ID NO:1669:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

1210

(A) NAME/KEY: misc_feature
(B) LOCATION 1...468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1667

```

Ile Tyr Ser Lys Thr Arg Ser His Asp Met Asp Ile Ser Ile Phe Arg
1      5      10      15
Glu Tyr Asp Ile Arg Gly Ile Tyr Pro Thr Thr Leu Asp Glu Asn Thr
      20      25      30
Ala Phe Ser Ile Gly Val Glu Leu Gly Lys Ile Met Arg Glu Tyr Asp
      35      40      45
Lys Ser Val Phe Val Gly His Asp Ala Arg Val His Gly Arg Phe Leu
      50      55      60
Phe Glu Val Leu Ser Ala Gly Leu Gln Ser Ser Gly Leu Lys Val Tyr
      65      70      75      80
Asp Leu Gly Leu Ile Pro Thr Pro Val Ala Tyr Phe Ala Ala Phe Asn
      85      90      95
Glu Ile Asp Asn Ile Gln Cys Pro Asn Ser Ile Met Ile Thr Gly Ser
      100      105      110
His Asn Pro Lys Glu Tyr Asn Gly Phe Lys Ile Thr Leu Asn Gln Asn
      115      120      125
Pro Phe Tyr Gly Lys Asp Ile Gln Ala Leu Lys Asn Thr Leu Leu Asn
      130      135      140
Ala Lys His Glu Ile Lys Pro Leu Lys Glu Thr Pro Glu Lys Val Asn
      145      150      155      160
Ala Leu Glu Ala Tyr His Arg Tyr Leu Ile Lys Asp Phe Lys His Leu
      165      170      175
Lys Asn Leu Lys Tyr Lys Ile Ala Leu Asp Phe Gly Asn Gly Val Gly
      180      185      190
Ala Leu Gly Leu Glu Pro Ile Leu Lys Ala Leu Asn Ile Asp Phe Ser
      195      200      205
Ser Leu Tyr Ser Asp Pro Asp Gly Asp Phe Pro Asn His His Pro Asp
      210      215      220
Pro Ser Glu Ala Lys Asn Leu Lys Asp Leu Glu Lys His Met Arg Glu
      225      230      235      240
Asn Ala Ile Leu Ile Gly Phe Ala Phe Asp Gly Asp Ala Asp Arg Ile
      245      250      255
Ala Met Leu Ser Ser His His Ile Tyr Ala Gly Asp Glu Leu Ala Ile
      260      265      270
Leu Phe Ala Lys Arg Leu His Ala Gln Gly Ile Thr Pro Phe Val Ile
      275      280      285
Gly Glu Val Lys Cys Ser Gln Val Met Tyr Asn Ala Ile Asn Thr Phe
      290      295      300
Gly Lys Thr Leu Met Tyr Lys Thr Gly His Ser Asn Leu Lys Ile Lys
      305      310      315      320
Leu Lys Glu Thr Asn Ala His Phe Ala Ala Glu Met Ser Gly His Ile
      325      330      335
Phe Phe Lys Glu Arg Tyr Phe Gly Tyr Asp Asp Ala Leu Tyr Ala Cys
      340      345      350
Leu Arg Ala Leu Glu Leu Leu Leu Glu Gln Ser Pro Ser Asp Leu Glu
      355      360      365
Asn Thr Ile Lys Asn Leu Pro Tyr Ser Tyr Thr Thr Pro Glu Glu Lys
      370      375      380
Ile Ala Val Ser Glu Glu Lys Phe Glu Ile Ile Arg Asn Leu Gln
      385      390      395      400
Glu Ala Leu Lys Asn Pro Pro Ser His Phe Pro Thr Ile Lys Glu Ile
      405      410      415
Ile Ser Ile Asp Gly Val Arg Val Val Phe Glu His Gly Phe Gly Leu
      420      425      430
Ile Arg Ala Ser Asn Thr Thr Pro Tyr Leu Val Ser Arg Phe Glu Gly
      435      440      445
Lys Asp Glu Thr Thr Ala Leu Glu Tyr Lys Arg Ala Leu Leu Gly Leu
      450      455      460
Leu Glu Lys Leu
465

```

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1209

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1666

```

Asn Pro Ala Leu Ser Leu His Thr Trp Leu Pro Tyr Ala Tyr Ser Asn
1      5      10      15
Ala Pro Thr Leu Gly Ser Val Met Leu Ser Ala Leu Leu Ser Lys Met
20      25      30
Gly Thr Tyr Ala Leu Leu Arg Phe Leu Leu Pro Leu Phe Pro Glu Leu
35      40      45
Ser Glu Ile Tyr Leu Thr Pro Ile Ala Ile Val Ala Leu Cys Met Ile
50      55      60
Ile Tyr Gly Gly Phe Leu Ala Tyr Ala Gln Lys Asp Leu Lys Thr Leu
65      70      75      80
Ile Ala Tyr Ser Ser Phe Ser His Met Gly Val Val Val Leu Gly Val
85      90      95
Phe Ser Phe Asn Val Glu Gly Val Ser Gly Ala Val Phe Met Met Phe
100     105     110
Ala His Gly Val Ile Val Met Gly Leu Phe Leu Leu Ala Gly Ile Leu
115     120     125
Glu Glu Arg Ala Ser Ser Leu Glu Ile Ala Arg Phe Gly Ser Ile Ala
130     135     140
Lys Ser Ala Pro Val Phe Ala Ala Phe Phe Met Ile Val Leu Met Ala
145     150     155     160
Asn Val Gly Met Pro Leu Ser Ile Gly Phe Val Gly Glu Phe Leu Ser
165     170     175
Leu Leu Gly Phe Phe Ala Thr Tyr Pro Leu Leu Ala Ile Ile Ala Gly
180     185     190
Thr Ser Ile Ile Leu Ser Ala Val Tyr Met Leu Thr Ser Tyr Lys Asp
195     200     205
Val Phe Phe Gly Asn Leu Lys Thr Gly Asn Asn Gln Ile Ser Val Phe
210     215     220
Glu Asp Leu Asn Ala Arg Glu Val Gly Val Leu Ser Val Ile Leu Ala
225     230     235     240
Leu Ile Leu Ile Leu Gly Ile Tyr Pro Lys Ala Leu Leu Lys Pro Ile
245     250     255
Glu Gln Gly Phe Lys Gln Leu Leu Glu Val Ile Glu Ile Arg Ser Leu
260     265     270
Leu Phe Leu Gly Ser Leu Asp Thr Lys Ile Lys Glu Val Ser Tyr Val
275     280     285
Asn Arg Tyr Ser Pro His Leu Phe
290     295

```

(2) INFORMATION FOR SEQ ID NO:1667:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

1208

65		70		75		80									
Leu	Asp	Thr	Leu	Ser	Leu	Ile	Ser	Gln	Ser	Ile	Val	Leu	Ile	Ser	Ala
			85						90					95	
Phe	Phe	Leu	Ile	Phe	Leu	Ala	Leu	Ser	Lys	Glu	Arg	Phe	Asn	Glu	Phe
		100						105					110		
Gln	Thr	Ala	Glu	Phe	Tyr	Ser	Leu	Tyr	Leu	Phe	Ile	Val	Ala	Gly	Phe
		115					120					125			
Gln	Phe	Met	Val	Ser	Ser	Asn	Gln	Phe	Val	Val	Ile	Leu	Ile	Gly	Leu
	130					135					140				
Glu	Thr	Ala	Pro	Leu	Pro	Leu	Cys	Val	Leu	Met	Ala	Leu	Ser	Asp	Lys
145				150						155					160
Arg	Tyr	Gly	Leu	Glu	Ala	Gly	Ile	Lys	Tyr	Phe	Thr	Met	Gly	Ala	Met
			165					170						175	
Ala	Ser	Ala	Phe	Phe	Ala	Met	Gly	Ala	Met	Ala	Phe	Tyr	Leu	Leu	Thr
			180					185					190		
Gly	Ser	Leu	Asn	Leu	Glu	Val	Ile	Thr	Leu	Tyr	Leu	His	Thr	Glu	Gly
	195						200					205			
Ile	Thr	Asn	Pro	Met	Leu	Phe	Ala	Met	Gly	Thr	Ile	Phe	Leu	Ile	Gly
	210					215						220			
Ala	Ile	Gly	Phe	Lys	Val	Ser	Leu	Val	Pro	Phe	His	Thr	Trp	Met	Pro
225				230						235					240
Asp	Val	Tyr	Glu	Gly	Asn	Asn	Pro	Val	Phe	Ala	Ser	Tyr	Ile	Ser	Ile
			245						250					255	
Val	Pro	Lys	Ile	Ala	Gly	Phe	Val	Val	Ala	Thr	Arg	Leu	Phe	Gly	Ala
		260					265						270		
Phe	Ile	Asp	Thr	His	Thr	Ala	Trp	Val	Glu	Asp	Ile	Phe	Tyr	Val	Leu
		275					280					285			
Ile	Leu	Met	Thr	Ile	Thr	Ile	Pro	Asn	Phe	Ile	Ala	Leu	Trp	Gln	Glu
	290					295					300				
Asp	Val	Lys	Arg	Met	Leu	Ala	Tyr	Ser	Ser	Ile	Ser	His	Ser	Gly	Phe
305				310						315					320
Ala	Leu	Ala	Cys	Val	Phe	Ile	His	Thr	Glu	Asp	Ser	Gln	Gln	Ala	Met
			325						330					335	
Phe	Val	Tyr	Trp	Phe	Met	Phe	Ala	Phe	Thr	Tyr	Ile	Gly	Ala	Phe	Gly
		340					345					350			
Leu	Leu	Trp	Leu	Leu	Lys	Ser	Arg	Glu	Lys	Thr	Trp	Asp	Glu	Arg	Tyr
		355				360						365			
Asp	His	Pro	Tyr	Ser	Lys	Phe	Asn	Gly	Leu	Ile	Lys	Thr	His	Pro	Leu
	370					375					380				
Val	Ala	Ile	Leu	Gly	Ala	Ile	Phe	Val	Phe	Gly	Leu	Ala	Gly	Ile	Pro
385				390						395					400
Pro	Phe	Ser	Val	Phe	Trp	Gly	Lys	Phe	Leu	Ala	Val	Glu	Ser	Ala	Leu
			405						410					415	
Glu	Ser	Asn	His	Ile	Leu	Leu	Ala	Val	Val	Met	Leu	Val	Asn	Ser	Ala
			420				425					430			
Val	Ala	Ala	Phe	Tyr	Tyr	Phe	Arg	Trp	Leu	Val	Ala	Met	Phe	Phe	Asn
		435					440					445			
Lys	Pro	Leu	Gln	Thr	Gln	Ser	Tyr	Ala	Gln	Asn	Asp	Ile	Tyr	Thr	Gln
	450					455					460				
Asn	Ala	Thr	Met	Pro	Ile	Tyr	Ala	Val	Ile	Ile	Ala	Met	Ala	Leu	Ala
465				470						475					480
Cys	Leu	Phe	Ser	Val	Phe	Met	Met	Arg	Gly	Leu	Leu	Glu	Phe	Val	Ala
			485						490					495	

(2) INFORMATION FOR SEQ ID NO:1666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1664

```

Glu Met Gln Phe Leu His Ala His Leu Leu Ser Val Val Ile Phe Phe
1      5      10      15
Pro Met Leu Ser Ala Leu Leu Ala Phe Phe Met Ser Asp Gln Ala Ser
      20      25      30
Arg Ala Tyr Ala Ile Val Ile Ala Leu Ile Glu Leu Leu Leu Val Leu
      35      40      45
Leu Leu Trp His Gly Phe Asp Ile Gln Thr Ala Gly Met Gln Phe Glu
50      55      60
Glu Met Lys Glu Leu Ala Tyr Gln Ile Gly Val Asn Tyr His Val Gly
65      70      75      80
Val Asp Gly Ile Ala Leu Phe Leu Leu Leu Asn Ala Ile Val Val
      85      90      95
Leu Leu Ser Val Ile Tyr Val Lys Glu Arg Arg Lys Asp Phe Val Ile
100      105      110
Cys Leu Leu Leu Leu Glu Gly Ile Leu Met Gly Val Phe Ser Ser Leu
115      120      125
Asn Val Ile Phe Phe Tyr Ala Phe Trp Glu Ile Ser Leu Leu Pro Val
130      135      140
Leu Tyr Leu Ile Gly Arg Phe Gly Arg Asn Asn Lys Ile Tyr Ser Gly
145      150      155      160
Met Lys Phe Phe Leu Tyr Thr Phe Leu Ala Ser Leu Cys Met Leu Leu
      165      170      175
Gly Ile Leu Tyr Ile Gly Tyr Asp Tyr Ala Asn Asn Tyr Gly Met Met
180      185      190
Ser Phe Asp Ile Leu Asp Trp Tyr Gln Leu Asn Phe Ser Ser Gly Ile
195      200      205
Lys Thr Trp Leu Phe Val Ala Phe Leu Ile Gly Ile Ala Val Lys Ile
210      215      220
Pro Leu Phe Pro Phe Thr His Gly Cys Leu Met Arg Ile Leu Thr Pro
225      230      235      240
Pro Leu

```

(2) INFORMATION FOR SEQ ID NO:1665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...496

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1665

```

Lys Arg Ser Leu Met Leu Ile Asp Ile Leu His Ile Ser Phe Asp Ser
1      5      10      15
Phe Ser Phe Glu Ser Ile Leu Pro Met Leu Val Leu Val Cys Gly Gly
      20      25      30
Ile Phe Thr Leu Leu Ile Asn Ala Phe Thr Ser Arg Phe Ser Arg Asn
      35      40      45
Leu Asn Val Phe Leu Cys Met Leu Phe Leu Val Leu Asp Phe Leu Val
50      55      60
Val Ser Gly Leu Glu Glu Gln Glu Asn Ala Phe Phe Gly Phe Leu Ser

```

1206

```

Arg Arg Asn Leu Thr Arg Gln His Gly Ser Val Lys Lys Arg Glu Lys
1           5           10           15
Arg Phe Lys Thr His Ala Ser Leu Cys Asp Ser Val Arg Ser Gly Lys
          20           25           30
Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp Ile Val Asn Ile Gly
          35           40           45
Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val Cys Thr Ala Leu Lys
50           55           60
Arg Tyr Gly His Pro Arg Leu Glu Met His Phe Val Ser Asn Val Asp
65           70           75           80
Gly Thr Gln Ile Leu Asp Val
          85

```

(2) INFORMATION FOR SEQ ID NO:1663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1663

```

Gln His Tyr Pro Asn Asn Leu Lys Asp Ile Glu Met Asn Thr Glu Ile
1           5           10           15
Leu Thr Ile Met Leu Val Val Ser Val Leu Met Gly Leu Val Gly Leu
          20           25           30
Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln Phe Asp Asp Glu Lys
          35           40           45
Arg Met Leu Glu Ser Val Leu Tyr Asp Ser Ala Ser Asp Leu Asn Glu
50           55           60
Ala Ile Leu Gln Glu Lys Arg Gln Lys Asn
65           70

```

(2) INFORMATION FOR SEQ ID NO:1664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...242

1205

```

Ile Leu Leu Val Gln Thr Phe Phe Ser Phe Cys Val Leu Val Ala Glu
 50          55          60
Tyr Pro Ser Gly Val Leu Ala Asp Leu Met Ser Arg Lys Asn Leu Phe
 65          70          75          80
Leu Val Ser Asn Val Phe Leu Ile Ala Ser Phe Ser Phe Val Leu Phe
          85          90          95
Phe Asp Ser Phe Ile Leu Met Leu Leu Ala Trp Gly Leu Tyr Gly Leu
          100          105          110
Tyr Ser Ala Cys Ser Ser Gly Thr Ile Glu Ala Ser Leu Ile Thr Asp
          115          120          125
Ile Lys Glu Asn Lys Lys Asp Leu Ser Lys Phe Leu Ala Lys Asn Asn
 130          135          140
Gln Ile Thr Tyr Leu Gly Met Ile Ile Gly Ser Ser Leu Gly Ser Phe
 145          150          155          160
Leu Tyr Leu Lys Val His Ala Met Leu Tyr Val Val Gly Ile Phe Leu
          165          170          175
Ile Met Leu Cys Ala Leu Thr Ile Ile Ile Tyr Phe Lys Glu Lys Glu
          180          185          190
Gly Asp Phe Lys Ser Gln Lys Asn Leu Lys Leu Leu Lys Glu Gln Val
 195          200          205
Lys Gly Ser Leu Lys Glu Leu Lys Asp Asn Pro Lys Leu Lys Ile Leu
 210          215          220
Leu Val Gly His Leu Ile Thr Pro Val Phe Phe Met Ser His Phe Gln
 225          230          235          240
Met Trp Gln Ala Tyr Phe Leu Lys Gln Gly Val Lys Glu Gln Tyr Leu
          245          250          255
Phe Val Phe Tyr Ile Ala Phe Gln Val Ile Ser Ile Leu Ile His Phe
          260          265          270
Leu Lys Ala Lys Asn Tyr Ser Gln Lys Ile Ala Leu Ser Ser Leu Leu
          275          280          285
Val Leu Leu Gly Val Ser Pro Leu Leu Leu Ser Asn Ile Pro Tyr Cys
 290          295          300
Phe Ile Gly Val Tyr Ala Leu Met Val Ala Phe Phe Ala Tyr Met Ser
 305          310          315          320
Tyr Cys Leu Gly Tyr Gln Phe Ser Lys Phe Val Ser Lys Asn Asn Ile
          325          330          335
Ser Ser Leu Ser Ser Leu Leu Ser Ser Cys Val Arg Val Val Ser Val
          340          345          350
Leu Ile Leu Ser Leu Ser Ser Leu Glu Leu Arg Tyr Phe Ser Pro Leu
          355          360          365
Thr Ile Ile Thr Met His Phe Ala Leu Thr Leu Ile Ile Leu Phe Phe
 370          375          380
Phe Leu Tyr Lys Ala Lys Pro Phe Asp Glu
 385          390

```

(2) INFORMATION FOR SEQ ID NO:1662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1662

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1204

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1660

```

Lys Arg Ile Lys Arg Gly Phe Phe Met Gln Glu Ala Leu Leu Arg Phe
1      5      10      15
Gln Glu Gly Phe Lys Glu Trp Gly Tyr Leu Ile Leu Phe Leu Tyr Ser
      20      25      30
Leu Gly Gly Gly Tyr Val Gly Ile Val Ile Ala Ser Ile Leu Ser Ala
      35      40      45
Thr Thr His Ala Leu Asp Ile Lys Ile Thr Ile Leu Val Ala Phe Leu
50      55      60
Gly Asn Leu Ile Gly Ser Gly Ala Leu Val Ile Phe Ala Arg Tyr Gln
65      70      75      80
Lys Arg Glu Phe Leu Lys Tyr Phe Gln Lys His Arg Arg Lys Leu Ala
      85      90      95
Leu Ala Ser Leu Trp Val Lys Arg Tyr Ala Leu Leu Met Ile Phe Val
      100      105      110
Asn Lys Tyr Leu Tyr Gly Ile Lys Ser Val Val Pro Leu Ala Ile Gly
      115      120      125
Phe Ser Lys Tyr Pro Leu Lys Lys Phe Leu Trp Leu Asn Val Phe Ser
130      135      140
Ser Phe Leu Trp Ala Leu Ile Val Gly Ser Val Ser Phe Gln Ala Ser
145      150      155      160
Asp Trp Val Lys Thr Leu Tyr Glu Arg Leu Ser His Tyr Thr Ser Phe
      165      170      175
Phe Val Ile Ser Phe Val Leu Ile Ala Leu Leu Ile Trp Phe Leu Leu
      180      185      190
Lys Arg Tyr Ser Arg Lys Met Gly Phe
      195      200

```

(2) INFORMATION FOR SEQ ID NO:1661:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1661

```

Ala Ser Phe Asn Tyr Asn Phe Gln Met Leu Arg Lys Asn Ile Leu Ala
1      5      10      15
Tyr Tyr Gly Ala Asn Phe Leu Leu Ile Ala Gln Ser Leu Pro His
      20      25      30
Ala Ile Leu Thr Pro Leu Leu Leu Ser Lys Gly Leu Ser Leu Ser Glu
      35      40      45

```

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```

Leu Gly Glu Thr Arg Val Ala Ser Ile Thr Ile Phe Asn Glu Ala Glu
      180      185      190
Ala Leu Asn Tyr Ser Lys Ala His Gln Tyr Ala Leu Thr Leu Thr Leu
      195      200      205
Ile Ser Phe Ser Leu Leu Phe Val Thr Leu Phe Leu Asn Lys Lys Gln
      210      215      220
Ser Ser Phe Leu
225

```

(2) INFORMATION FOR SEQ ID NO:1659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1659

```

Asn Phe Ile Phe Gly Glu Phe Ile Met Lys Arg Ser Ser Val Phe Ser
1      5      10      15
Phe Leu Val Ala Phe Leu Leu Val Val Gly Cys Ser His Lys Met Asp
      20      25      30
Asn Lys Thr Val Ala Gly Asp Val Ser Thr Lys Ala Val Gln Thr Ala
      35      40      45
Pro Val Thr Thr Glu Pro Ala Pro Glu Lys Glu Glu Pro Lys Gln Glu
      50      55      60
Pro Ala Pro Val Val Glu Glu Lys Pro Ala Ile Glu Ser Gly Thr Ile
65      70      75      80
Ile Ala Ser Ile Tyr Phe Asp Phe Asp Lys Tyr Glu Ile Lys Glu Ser
      85      90      95
Asp Gln Glu Thr Leu Asp Glu Ile Val Gln Lys Ala Lys Glu Asn His
      100      105      110
Met Gln Val Leu Leu Glu Gly Asn Thr Asp Glu Phe Gly Ser Ser Glu
      115      120      125
Tyr Asn Gln Ala Leu Gly Val Lys Arg Thr Leu Ser Val Lys Asn Ala
      130      135      140
Leu Val Ile Lys Gly Val Glu Lys Asp Met Ile Lys Thr Ile Ser Phe
145      150      155      160
Gly Glu Ser Lys Pro Lys Cys Val Gln Lys Thr Arg Glu Cys Tyr Arg
      165      170      175
Glu Asn Arg Arg Val Asp Val Lys Leu Val Lys
      180      185

```

(2) INFORMATION FOR SEQ ID NO:1660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1202

```

145          150          155          160
Asp Glu Lys Ile Thr Pro Phe Lys Glu Val Tyr Ala Lys Gly Val
      165          170          175
Leu Val Leu Trp Ser Glu Asn Leu Lys Met Asp Ser Leu Glu Ile Leu
      180          185          190
Lys Asp Pro Lys Ile Lys Arg Ile Ala Met Ala Asn Pro Lys Leu Ala
      195          200          205
Pro Tyr Gly Lys Ala Ser Met Glu Val Leu Asp Arg Leu Lys Leu Thr
      210          215          220
Pro Ser Leu Lys Ser Lys Ile Ile Tyr Gly Ala Ser Ile Ser Gln Ala
225          230          235          240
His Gln Phe Ile Ala Thr Lys Asn Ala Gln Ile Gly Phe Gly Ala Leu
      245          250          255
Ser Leu Ile Asp Lys Lys Asp Lys Asn Leu Ser Tyr Phe Ile Ile Asp
      260          265          270
Lys Thr Leu Tyr Asn Pro Ile Glu Gln Ala Leu Ile Ile Thr Lys Asn
      275          280          285
Gly Ala Asn Asn Pro Leu Ala Lys Val Phe Lys Asp Phe Leu Phe Ser
      290          295          300
Pro Lys Ala Arg Ala Ile Phe Lys Glu Tyr Gly Tyr Ile Val Asp
305          310          315

```

(2) INFORMATION FOR SEQ ID NO:1658:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...228

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1658

```

Lys Arg Arg Thr Met Asp His Glu Phe Leu Ile Thr Met Arg Leu Ser
1          5          10          15
Phe Ser Leu Ala Leu Ile Thr Thr Leu Ile Leu Leu Pro Ile Gly Ile
      20          25          30
Phe Leu Gly Tyr Phe Leu Ser Leu Lys Arg Asn Leu Leu Thr Ser Leu
      35          40          45
Thr Glu Thr Leu Val Tyr Met Pro Leu Val Leu Pro Pro Ser Val Leu
      50          55          60
Gly Phe Tyr Leu Leu Leu Ile Phe Ser Pro Ser Ser Phe Leu Gly Ala
65          70          75          80
Phe Leu Gln Asp Val Leu Asn Val Lys Leu Val Phe Ser Phe Gln Gly
      85          90          95
Leu Ile Leu Gly Ser Val Ile Phe Ser Leu Pro Phe Met Val Ser Pro
      100          105          110
Ile Lys Ser Ala Leu Ile Ser Leu Pro Thr Ser Leu Lys Glu Ala Ser
      115          120          125
Tyr Ser Leu Gly Lys Gly Glu Tyr Tyr Thr Leu Phe Phe Val Leu Leu
      130          135          140
Pro Asn Ile Lys Pro Ser Val Leu Met Ala Ile Ile Thr Thr Phe Met
145          150          155          160
His Thr Ile Gly Glu Phe Gly Val Val Met Met Leu Gly Gly Asp Ile
      165          170          175

```

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1201

Glu Ile Asp Thr Ser Ser Leu Ile Ser Val Glu Gly Asn Val Glu Gly
 65 70 75 80
 Tyr Glu Thr Phe Ser Asp Ser Leu Phe Leu Leu Ser Lys Glu Arg Ile
 85 90 95
 Glu Glu Ala Leu His Tyr Tyr Gln Pro Lys Lys Val Tyr Asn Leu Ser
 100 105 110
 Tyr Gly Ala Lys Ile Lys His Ala Val Ser Leu Asn His Ser Gln Val
 115 120 125
 Lys Leu Lys Gln Ile Asn Lys Gln Asp Ala Ile Val Arg Ile Lys Ser
 130 135 140
 Met Phe Ser Pro Arg Ser Asn His Ala Lys Asp Leu Lys Asn Leu Gln
 145 150 155 160
 Lys Asn Leu Ile Arg Phe Lys Glu Asp Phe Phe Thr His Leu Asn Thr
 165 170 175
 Pro Cys Lys Thr Lys Gln Glu Ala Phe Glu Trp Val Asp Ser Leu Ser
 180 185 190
 Gly Phe Cys Gln Thr Ala Ser Ala Lys Thr Pro Thr Ile Gly Ile Leu
 195 200 205
 Phe Glu Gly Ser Val Ala His Ile Leu Gln Ser Val Leu Ile Val Ser
 210 215 220
 Leu His Leu Lys Glu Asn Glu Leu Thr Leu Leu Ser Asn Ser Leu Lys
 225 230 235 240
 Thr Pro

(2) INFORMATION FOR SEQ ID NO:1657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1657

Ile Leu Leu Val Glu Leu Lys Leu His Pro Lys Ile Gly Tyr Phe Ser
 1 5 10 15
 Lys Arg Phe Asn Phe Leu Ser Lys Met Arg Val Leu Glu Trp Lys Tyr
 20 25 30
 Trp Leu Asn Thr Asp Lys Trp Asp Thr Pro Thr Asn Lys Pro Pro Gln
 35 40 45
 Thr Phe Lys Ile Gln Ile Phe Lys Ile Gln Ile Gly Ile Ile Asn Asn
 50 55 60
 Phe Asn His Leu Ile Lys Gly Ser Ser Met Lys Asn Ala Phe Lys Ala
 65 70 75 80
 Phe Ala Leu Leu Ile Val Phe Phe Ser Asn Ala Leu Leu Ala Gln Asp
 85 90 95
 Leu Lys Ile Ala Ala Ala Asn Leu Thr Arg Ala Leu Lys Ala Leu
 100 105 110
 Val Lys Glu Phe Gln Lys Glu His Pro Lys Asp Ala Ile Asn Ile Ser
 115 120 125
 Phe Asn Ser Ser Gly Lys Leu Tyr Ala Gln Ile Ala Gln Asn Ala Pro
 130 135 140
 Phe Asp Leu Phe Ile Ser Ala Asp Ile Ala Arg Pro Lys Lys Leu Tyr

SUBSTITUTE SHEET (RULE 26)

1200

```

      85              90              95
Ile Lys Gln Glu Val Leu Val Phe Gly Leu Leu Gln Val Val Leu Cys
      100              105              110
Ala Leu Ile Ala Phe Leu Leu Gly Tyr Phe Val Leu Gly Leu Ser Pro
      115              120              125
Ile Phe Ser Leu Val Leu Gly Met Gly Leu Ser Leu Ser Ser Thr Ala
      130              135              140
Ile Val Leu Lys Phe Phe Glu Asp Ser Lys Gln Leu Ser Thr Pro Met
      145              150              155              160
Gly Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile
      165              170              175
Pro Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val
      180              185              190
Asn Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile
      195              200              205
Leu Leu Leu Leu Pro Glu Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln
      210              215              220
Ala Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Val Leu Val
      225              230              235              240
Ile Val Cys Ser Ala Ala Gly Leu Ser His Phe Phe Gly Phe Ser Met
      245              250              255
Ser Leu Gly Ala Phe Ile Val Gly Met Ala Ile Ser Lys Ser Arg Tyr
      260              265              270
Lys Ile Asn Val Gln Glu Glu Phe Ala Gln Leu Lys Asn Leu Phe Leu
      275              280              285
Ala Leu Phe Phe Ile Thr Ile Gly Met Gln Ile Asn Val Ser Phe Phe
      290              295              300
Met Glu Lys Phe Phe Val Val Ile Phe Leu Leu Ile Leu Val Met Ser
      305              310              315              320
Phe Lys Thr Phe Ile Ile Tyr Ala Leu Leu Arg Phe Phe Arg Asp Ala
      325              330              335
Lys Thr Ala Ile Lys Thr Ala Leu Ser Leu Ala Gln Ile Gly Glu Phe
      340              345              350
Ser Phe Val Ile Phe Leu Asn Ser Ala Leu Ala Pro Ala Leu
      355              360              365

```

(2) INFORMATION FOR SEQ ID NO:1656:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1656

```

Cys Leu Cys Val Gly Gly Ala Leu Ala His Ile Ser Pro Leu Ser Ile
1      5      10      15
Glu Tyr Ala Ala Pro Phe Val Gly Asn Ala Gly Val Ala Leu Ala Gly
      20      25      30
Leu Met Ser Asp Glu Ile Tyr Leu Cys Ala Leu Asp Cys Ala Tyr Ile
      35      40      45
Lys Gly Phe Lys Lys His Ala Gln Asn Ser Tyr Tyr Gly Asp Glu Lys
50      55      60

```

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1199

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1654

```

Gly Val Thr Leu Ile Gln Gln Glu Gly Phe Ile Met Ile Lys Arg Ile
1           5           10           15
Ala Cys Ile Leu Ser Leu Ser Ala Ser Leu Ala Leu Ala Gly Glu Val
          20           25           30
Asn Gly Phe Phe Met Gly Ala Gly Tyr Gln Gln Gly Arg Tyr Gly Pro
          35           40           45
Tyr Asn Ser Asn Tyr Ser Asp Trp Arg His Gly Asn Asp Leu Tyr Gly
          50           55           60
Leu Asn Phe Lys Leu Gly Phe Val Gly Phe Ala Asn Lys Trp Phe Gly
          65           70           75           80
Ala Arg Val Tyr Gly Phe Leu Asp Trp Phe Asn Thr Ser Gly Thr Glu
          85           90           95
His Thr Lys Thr Asn Leu Leu Thr Tyr Gly Gly Gly Gly Asp Leu Ile
          100          105          110
Val Asn Leu Ile Pro Ser Asp Lys Phe Ala Leu Gly Leu Ile Gly Gly
          115          120          125
Val Gln Leu Ala Gly Asn Thr Trp Met Phe Pro Tyr Asp Val Asn Gln
          130          135          140
Thr Arg Phe Gln Phe Leu Trp Asn Leu Gly Gly Arg Met Arg Val Gly
          145          150          155          160
Asp Arg Ser Ala Phe Glu Ala Gly Val Lys Phe Pro Met Val Asn Gln
          165          170          175
Gly Ser Lys Asp Val Gly Leu Ile Arg Tyr Tyr Ser Trp Tyr Val Asp
          180          185          190
Tyr Val Phe Thr Phe
          195

```

(2) INFORMATION FOR SEQ ID NO:1655:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1655

```

Phe Arg Phe Tyr Phe Phe Lys Ala Asn Arg Ser Tyr Trp Gly Lys Val
1           5           10           15
Phe Met Val Asn Ser Thr Leu Tyr Ile Val Ile Ala Gly Leu Trp Leu
          20           25           30
Ala Val Gly Phe Gly Ile Phe Leu Lys Lys Leu Asp Met Pro Val Ile
          35           40           45
Ile Gly Tyr Ile Cys Thr Gly Thr Val Leu Ala Ala Phe Phe Lys Ile
          50           55           60
Asn Asp Phe Asn Leu Leu Ser Asp Ile Gly Glu Phe Gly Ile Val Phe
          65           70           75           80
Leu Met Phe Met Ile Gly Ile Glu Phe Asn Phe Asp Lys Leu Lys Ser

```

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	20		25		30
Tyr	Gly	Asn	Lys	Ile	Ala
	35			40	
Gln	Gly	Arg	Tyr	Ile	Lys
	50			55	
Phe	Lys	Ser	Cys	Ser	Cys
	65			70	
Ser	Ser	Arg	Ala	Pro	Ile
			85		
Cys	Thr	Asn	Gln	Gly	Phe
			100		
Phe	Glu	Phe	Leu	Tyr	Tyr
	115			120	
Asn	Ile	Gly	Gly	Gly	Thr
	130			135	
Gly	Leu	Phe	Gln	Val	Lys
	145			150	
Ile	Ala	His	Thr	Leu	Ser
			165		
Lys	Ile	Asn	Glu	Leu	Leu
			180		
Tyr	Phe	Val	Arg	Phe	Asp
	195			200	
Thr	Ser	Gly	Gly	Lys	Met
	210			215	
Pro	Asn	Asp	Phe	Lys	Val
	225			230	
Ser	Gly	Ser	Gln	Pro	Pro
			245		
Gly	Tyr	Ile	Arg	Phe	Ile
	260			265	
Val	Thr	Tyr	Ile	Pro	Ile
	275			280	
Asp	Ile	Met	Met	Asp	Lys
	290			295	
Leu	Gln	Gly	Ala	Tyr	Asn
	305			310	
Gln	Ser	Met	Gln	Glu	Tyr
			325		
Lys	Lys	Tyr	Leu	Ser	Asn
			340		
Asn	Glu	Asn	His	Ile	Tyr
	355			360	
Leu	Leu	Gln	Lys	Tyr	Glu
	370			375	
Ile	Lys	Asn	Asn	Gln	Ser
	385			390	
Leu	Leu	Pro	Leu	Leu	Lys
			405		
				410	

(2) INFORMATION FOR SEQ ID NO:1654:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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His Leu Ser Leu His Tyr Leu Lys Ser Gln Asn Asn His Lys Leu Pro
 100 105 110
 Leu Thr Leu Lys Ala Thr His Ala Ile Ser Asn Phe Leu Asp Asn His
 115 120 125
 Gln Thr Pro Cys Ser Leu Lys Phe Leu Pro Pro Thr Met Ile Tyr
 130 135 140
 Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala Gln Asn Tyr
 145 150 155 160
 Arg Phe His Ser Leu Tyr Leu Phe Glu Glu Asn Leu Asp Leu Phe Lys
 165 170 175
 Ile Ser Cys Tyr Phe Ala Arg Tyr Glu Asp Leu Ile Lys Lys Gly Ala
 180 185 190
 Lys Leu Phe Ile Gln Gly Phe Phe Asn Pro Asn Glu Leu Lys Met Asp
 195 200 205
 Phe Leu Lys Arg Pro Ile Thr His Ser Phe Leu Lys Leu Glu Ile Met
 210 215 220
 Pro Tyr Lys Ser Ala Phe Asn Leu Arg Met Arg Glu Asn Ile Gln Ser
 225 230 235 240
 Tyr Tyr Lys Gln Ala Leu Arg Gly Trp Gly Ser Phe Glu Asp Glu Leu
 245 250 255
 Leu Gly Val Lys Asn Thr Leu Lys Asn Leu Pro Leu Cys Gln Thr Leu
 260 265 270
 Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val Val Gly Asn
 275 280 285
 Gly Pro Ser Leu Asp Leu Leu Asp Phe Leu Lys Glu Asn Glu Glu
 290 295 300
 Lys Phe Ile Ile Phe Ser Cys Gly Thr Ala Leu Lys Pro Leu Lys Ala
 305 310 315 320
 His Gly Val Lys Val Asp Phe Gln Ile Glu Val Glu Arg Ile Asp Tyr
 325 330 335
 Leu Lys Glu Val Leu Glu Arg Ala Pro Leu Glu Asp Thr Pro Leu Met
 340 345 350
 Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala Lys Glu Ala
 355 360 365
 Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Tyr Lys Pro Phe Glu
 370 375 380
 Tyr Arg Ile Arg Ser Ala Phe Cys Gly Gln Cys Arg Gly Gly Phe Ser
 385 390 395 400
 Gly Phe Asp Glu Arg
 405

(2) INFORMATION FOR SEQ ID NO:1653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 413 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...413

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1653

Lys Gly Leu Gly Leu Ser Glu Trp Gln Thr Phe Cys Leu Lys Asp Leu
 1 5 10 15
 Gly Lys Ile Val Gly Gly Ala Thr Pro Pro Thr Asn Asn Pro Lys Asn

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1651

```

Ala Lys Glu Leu Leu Asn Glu Pro Val Asp Lys Lys Glu Asn Phe Glu
1      5      10      15
Ser Leu Cys Gln Glu Ile Ala Asp His Thr His Gly Glu Tyr Thr Lys
20      25      30
Arg Leu Lys Leu Val Glu Phe Leu Met Leu Leu Ala Tyr Ala Asp Gly
35      40      45
Ile Leu Asp Ser Lys Glu Lys Glu Leu Phe Leu Asp Val Gly Ala Phe
50      55      60
Leu Gln Ile Asp Asn Gln Asp Phe Asn Glu Leu Tyr Asp Asn Phe Glu
65      70      75      80
His Phe Asn Ser Ile Glu Ile Pro Met Ser Leu Glu Glu Ala Lys Asn
85      90      95
Leu Phe Glu Ile Gln Thr His Thr Thr Met Gln Asp Leu Glu Lys Lys
100      105      110
Ala Leu Asp Leu Ser Ala Pro Tyr Tyr His Lys Met Asn Asp Asn Lys
115      120      125
Arg Tyr Ser Glu Gln Asp Phe Ile Ser Leu Lys Lys Ile Ala Leu Ala
130      135      140
Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:1652:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1652

```

Met Pro Phe Leu Lys Ala Leu Ala Ser Phe Asp Ala Pro Phe Leu Glu
1      5      10      15
Lys Glu Ile Ser Lys Arg Phe Arg Asp Asn Leu Val Phe Phe Lys Ser
20      25      30
Tyr His Pro Asn Leu Phe Asn Ala Leu Asn Thr Pro Phe Lys Asn Tyr
35      40      45
Gln Leu Leu Phe Glu Thr Asn His Leu Asn Leu Leu His Thr Pro Thr
50      55      60
Asn Ala Leu Ser Tyr Pro Lys His Gln Met Ile Glu Thr Ala Phe Asn
65      70      75      80
Met Ala Lys Asn Pro Leu Asn Asn Pro Arg Trp Ser Leu Asp Asn Asn
85      90      95

```

1195

```

Ile Thr Glu Lys Asn Tyr Ser Leu Asn Pro Gly Gln Tyr Phe Thr Ile
      485                      490                      495
Glu Asp Thr Ser Glu Thr Ile Ser Gln Ala Glu Phe Glu Asn Leu Met
      500                      505                      510
Gln Gln Tyr Ser Ser Glu Leu Ala Ser Leu Phe Asp Glu Ser Gln Asn
      515                      520                      525
Leu Gln Gln Glu Ile Leu Glu Thr Leu Lys Gly Val Arg Phe Glu
      530                      535                      540

```

(2) INFORMATION FOR SEQ ID NO:1650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1650

```

Lys Gly Asp Phe Met Lys Glu Gln Glu Trp Asp Leu Ser Ala Leu Phe
1      5      10      15
Glu Asn Lys Glu Ser Ala Glu Glu Phe Leu Lys Thr Leu Gln Thr Glu
      20      25      30
Val Gln Glu Phe Glu Asn Ala Tyr Gln Asn Asn Leu Lys Asn Leu Asp
      35      40      45
Ala Ala Lys Phe Ala Asn Thr Leu Lys His Tyr Glu Asn Leu Ser Glu
      50      55      60
Lys Ile Ser Arg Ala Met Ala Tyr Ala Gln Leu Phe Ala Lys Asn
      65      70      75      80
Thr Lys Glu Ala Lys Phe Tyr Ser Gln Cys Glu Met Ala Cys Ala Asn
      85      90      95
Ile Gln Gln His Leu Leu Phe Phe Glu Ile Glu Phe Lys Asn Leu Asp
      100     105     110
Ala Lys Lys Gln Leu Ala Phe Ile Lys Lys Cys Lys Asp His Ala Phe
      115     120     125
Tyr Leu Asn Asn Leu Ile Glu Lys Lys Lys His Thr Leu Asn Leu Asp
      130     135     140
Glu Glu Lys Ile Ala Leu Ala Leu Ser Pro Val Gly Val Gly Ala Phe
      145     150     155     160
Ser Phe Val Met Asp Glu His Leu Phe Ser Leu Asn Ile Ser Leu His
      165     170     175
Arg Ile Asn Phe Lys Arg Arg Ile Asn Phe Ser Pro Leu Ala Gln Pro
      180     185     190

```

(2) INFORMATION FOR SEQ ID NO:1651:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1194

(A) NAME/KEY: misc_feature
(B) LOCATION 1...543

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1649

```

Met Pro Asn Asn Ala Leu Leu Gln Ile Lys Gln Asp Thr Leu Ser Leu
1      5      10      15
Ile Asp Asp Leu Lys Val Ile Cys Lys Asp Ala Gly Leu Ala Gly Asp
      20      25      30
Gly Asn Gly Tyr Lys Ile Ile Thr Gln Cys Phe Leu Tyr Lys Phe Leu
      35      40      45
Cys Asp Lys Phe Glu Phe Phe Phe Glu Gln Lys Phe Pro Asn Lys Thr
      50      55      60
Ile Arg Asp Tyr Lys Asp Phe Asn Glu Glu Glu Lys Glu Tyr Phe Phe
      65      70      75      80
Leu Thr Leu Ser Asp Lys Lys Leu Pro Lys Leu Ala Tyr Asp Glu Leu
      85      90      95
Leu Asn Tyr Leu Phe Glu Lys His Phe Tyr Asp Asn Asp Leu His Leu
      100      105      110
Lys Leu Asp Ala Ile Phe Asn Arg Ile Ser Ser Asn Asn Ala Glu Leu
      115      120      125
Phe Asn Thr Lys Ser Thr Asp Glu Thr Thr Ile Ala Leu Phe Glu Ser
      130      135      140
Val Ser Gln Tyr Ile Asn Glu Gly Ser Lys Arg Ala Asn Phe Thr Arg
      145      150      155      160
Ser Leu Leu Asp Lys Leu Lys Asn Phe Asn Phe Lys Gln Ala Phe Leu
      165      170      175
Asn Leu Gln Asn Gln Gln Gly Tyr Asp Phe Phe Ala Pro Ile Phe Glu
      180      185      190
Tyr Leu Leu Lys Asp Tyr Asn Asn Asn Ser Gly Gly Thr Tyr Ala Glu
      195      200      205
Tyr Tyr Thr Pro Leu Ser Ile Ala Ser Ile Ile Ala Lys Leu Leu Val
      210      215      220
Asn Lys Pro Thr Gln Ser Val Lys Ile Tyr Asp Pro Ser Ala Gly Thr
      225      230      235      240
Gly Thr Leu Leu Met Ala Leu Ala His Gln Ile Gly Thr Asp Ser Cys
      245      250      255
Thr Leu Tyr Ala Gln Asp Ile Ser Gln Lys Ser Leu Arg Met Leu Lys
      260      265      270
Leu Asn Leu Ile Leu Asn Asp Leu Thr His Ser Leu Arg His Ala Ile
      275      280      285
Glu Gly Asn Thr Leu Thr Asn Pro Tyr His Ser Lys Asp His Lys Gly
      290      295      300
Lys Met Asp Phe Ile Val Ser Asn Pro Pro Phe Lys Leu Asp Phe Ser
      305      310      315      320
Asn Glu His Ala Glu Ile Ser Gln Asn Lys Asn Asp Phe Phe Leu Gly
      325      330      335
Val Pro Asn Ile Pro Lys Asn Asp Lys Ser Lys Met Pro Ile Tyr Thr
      340      345      350
Leu Phe Phe Gln His Cys Leu Asn Met Leu Ser Pro Lys Gly Lys Gly
      355      360      365
Ala Ile Ile Val Pro Thr Gly Phe Ile Ser Ala Lys Ser Gly Val Asn
      370      375      380
Asn Lys Asn Val Arg His Leu Val Asp Glu Arg Leu Val Tyr Gly Val
      385      390      395      400
Ile Cys Met Pro Ser Gln Val Phe Ala Asn Thr Gly Thr Asn Val Ser
      405      410      415
Ile Ile Phe Phe Gln Lys Thr Pro Ser Ala Lys Glu Val Ile Leu Ile
      420      425      430
Asp Ala Ser Lys Leu Gly Glu Glu Tyr Thr Glu Asn Lys Asn Lys Lys
      435      440      445
Thr Arg Leu Arg Pro Ser Asp Met Asp Leu Ile Leu Glu Thr Phe Gln
      450      455      460
Asn Lys Ala Pro Lys Ser Asp Phe Cys Ala Leu Val Ser Phe Asp Glu
      465      470      475      480

```

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```

Phe Asn Gly Glu Gly Ser Glu Ile Val Ala Ile Gly Ile Phe Val Leu
   35               40               45
Ile Leu Phe Val Phe Phe Ile Arg Pro Val Ser Phe Gln Asp Pro Glu
   50               55               60
Lys Arg Glu Glu Tyr Ile Glu Arg Leu Lys Lys Asn His Glu Arg Lys
   65               70               75               80
Met Ile Leu Gln Asp Lys Gln Lys Glu Glu Gln Met Arg Leu Tyr Gln
               85               90               95
Ala Lys Lys Glu Arg Glu Ser Arg Gln Lys Gln Asp Leu Lys Glu Gln
               100               105               110
Met Lys Lys Tyr Ser
               115

```

(2) INFORMATION FOR SEQ ID NO:1648:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1648

```

Arg Lys Lys Met Glu Ile Ile Leu Leu Ile Val Ala Ala Val Val Leu
1      5      10      15
Phe Tyr Phe Tyr Asn Thr Leu Lys Glu Tyr Leu Lys Asn Pro Leu Asn
   20      25      30
Pro Lys Thr Lys Thr Glu Glu Tyr Asp Leu Lys Asn Asp Pro Tyr Leu
   35      40      45
Leu Val Gln Ser Ser Pro Leu Asp Lys Phe Lys Gln Thr Gln Ile Gly
   50      55      60
Ala Tyr Met Arg Leu Leu Lys Phe Leu Asp Ile Gln Lys Asn Ala Leu
   65      70      75               80
Asp Asn Ala Leu Arg Thr Leu Phe Ile His Glu Leu Glu Gln Pro Leu
               85               90               95
Asn Ser Glu Gln Gln Asn Leu Gly Gln Arg Ala Ser Gln
   100      105

```

(2) INFORMATION FOR SEQ ID NO:1649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

1192

```

      20      25      30
Leu Leu Lys Gly Trp Gly Ser Lys Ile Phe Phe Ile Asn Arg Lys Phe
      35      40      45
Val Leu Ala Gln Tyr Asn Pro Ser Val Ser Ile Phe Ile Leu Leu Asn
      50      55      60
Arg Val Phe Gly Val Gly Val
      65      70

```

(2) INFORMATION FOR SEQ ID NO:1646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1646

```

Ile Gln Arg Ser His Gln Leu Phe Asn Leu Gln Glu Lys Lys Gly Ile
1      5      10      15
Leu Gly Phe Leu His Gln Lys Asn Ile Leu Asn Ile Ala Gln Asn Asp
      20      25      30
Ile His Gln Leu Leu Ile Leu Met Val Val Phe Ser Met Leu Ala Thr
      35      40      45
Pro Phe Ile Leu Lys Tyr Leu Glu Ser Ile Ala Gln Phe Ile Leu His
      50      55      60
Gln Lys Ser Gln Glu Asn Glu Pro Ala Lys Lys
      65      70      75

```

(2) INFORMATION FOR SEQ ID NO:1647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1647

```

Gly Leu Met Arg Ile Ile Arg Leu Ser Phe Lys Met Asn Ala
1      5      10      15
Phe Leu Lys Leu Ala Leu Ala Ser Leu Met Gly Gly Leu Trp Tyr Ala
      20      25      30

```

1191

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1644

```

Lys Thr Lys Leu Val Phe Met Ile Lys Ala Arg Phe Lys Lys Arg Leu
1      5      10      15
Leu Gly Ser Arg Gly Ala Phe Asp Leu Asn Ile Asp Leu Glu Ile Lys
      20      25      30
Glu Ala Glu Val Val Ala Leu Leu Gly Glu Ser Gly Ala Gly Lys Ser
      35      40      45
Thr Ile Leu Arg Ile Leu Ala Gly Leu Glu Ala Val Ser Ser Gly Tyr
      50      55      60
Ile Glu Ala Asn His Ser Val Trp Leu Asp Thr Gln Lys Lys Ile Phe
      65      70      75      80
Leu Lys Pro Gln Gln Arg Lys Ile Gly Phe Val Phe Gln Asp Tyr Ala
      85      90      95
Leu Phe Pro His Leu Asn Val Tyr Gln Asn Ile Ala Phe Ala His Pro
      100     105     110
Lys Asp Lys Asn Lys Ile His Glu Val Leu Arg Leu Met Arg Leu Glu
      115     120     125
Asn Leu Ser Gln Gln Lys Ile Pro Lys Leu Ser Gly Gly Gln Ala Gln
      130     135     140
Arg Val Ala Leu Ala Arg Ala Leu Ile Ala Ala Lys Asn Leu Leu Leu
      145     150     155     160
Leu Asp Glu Pro Leu Asn Ala Leu Asp Asn Ala Leu Lys Asn Glu Val
      165     170     175
Gln Gln Gly Leu Leu Asp Phe Ile Lys Arg Glu Asn Leu Ser Val Leu
      180     185     190
Leu Val Ser His Asp Pro Asn Glu Ile Thr Lys Leu Ala Arg Thr Phe
      195     200     205
Leu Phe Leu Asn Asn Gly Val Ile Asp Pro Asn Gln Glu Asn Arg Leu
      210     215     220
Phe Ser Asn Arg Leu Leu Val Lys Pro Leu Phe Glu Asp Glu Asn Tyr
      225     230     235     240
Cys His Tyr Glu Val Ile Pro Gln Thr Ile Ser Leu Pro Lys Asp Cys
      245     250     255
Leu Asn Pro Thr Phe Lys Leu Asp Phe Ile Gln Asn Lys Lys Phe
      260     265     270

```

(2) INFORMATION FOR SEQ ID NO:1645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1645

```

Gly Leu Ser Ala Thr Ile Leu Gly Met Trp Ile Met Ser Ser Leu Ser
1      5      10      15
Ser Ser Phe Phe His Ser Leu Phe Phe Ile Lys Ser Asn Pro Gly Gln

```

1190

```

Ile Trp Arg Gly Cys Gly Ser His Asp Arg Val His Asp Glu Phe Val
1      5      10      15
Phe Ala Arg Tyr Thr Lys Ala Asn Tyr Glu Asn Thr Tyr Tyr Asp Thr
      20      25      30
Glu Phe Ser His Leu Lys Glu Ala Ser Ala Tyr Phe Pro Asp Ile Asp
      35      40      45
Glu Ala Ser Leu Phe Thr Asp Leu Gln Asp Tyr Phe Asn Ser Trp Lys
      50      55      60
Glu Leu Ser Lys Asn Ala Lys Asp Ser Ala Gln Lys Gln Ala Leu Ala
      65      70      75      80
Gln Lys Thr Glu Ala Leu Thr His Asn Ile Lys Asp Thr Arg Glu Arg
      85      90      95
Leu Thr Thr Leu Gln His Lys Ala Ser Glu Glu Leu Lys Ser Val Ile
      100     105     110
Lys Glu Val Asn Ser Leu Gly Ser Gln Ile Ala Glu Ile Asn Lys Arg
      115     120     125
Ile Lys Glu Val Glu Asn Asn Lys Ser Leu Lys His Ala Asn Glu Leu
      130     135     140
Arg Asp Lys Arg Asp Glu Leu Glu Phe His Leu Arg Glu Leu Leu Gly
      145     150     155     160
Gly Asn Val Phe Lys Ser Ser Ile Lys Thr His Ser Leu Thr Asp Lys
      165     170     175
Asp Ser Ala Asp Phe Asp Glu Ser Tyr Asn Leu Asn Ile Gly His Gly
      180     185     190
Phe Asn Ile Ile Asp Gly Ser Ile Phe His Pro Leu Val Val Lys Glu
      195     200     205
Ser Glu Asn Lys Gly Gly Leu Asn Gln Val Tyr Phe Gln Ser Asp Asp
      210     215     220
Phe Lys Leu Thr Asn Ile Thr Asp Lys Leu Asn Gln Gly Lys Val Gly
      225     230     235     240
Ala Leu Leu Asn Val Tyr Asn Asp Gly Ser Asn Gly Thr Leu Lys Gly
      245     250     255
Lys Leu Gln Asp Tyr Ile Asp Leu Leu Asp Ser Phe Ala Arg Gly Leu
      260     265     270
Ile Glu Ser Thr Asn Ala Ile Tyr Ala Gln Ser Ala Ser His His Ile
      275     280     285
Glu Gly Glu Pro Val Glu Phe Asn Ser Asp Glu Ala Phe Lys Asp Thr
      290     295     300
Asn Tyr Asn Ile Lys Asn Gly Ser Phe Asp Leu Ile Ala Tyr Asn Thr
      305     310     315     320
Asp Gly Lys Glu Ile Ala Arg Lys Thr Ile Ala Ile Thr Pro Ile Thr
      325     330     335
Thr Met Asn Asp Ile Ile Gln Val Ile Asn Ala Asn Thr Asp Asp Asn
      340     345     350
Gln Asp Asn Asn Thr Glu Asn Asp Phe Asp Glu Leu Phe His Ser Glu
      355     360     365
Leu

```

(2) INFORMATION FOR SEQ ID NO:1644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

1189

```

Thr Gln His Ser Val Gln Glu Leu Arg Arg Leu Gly Val Thr Pro Gln
195 200 205
Ile Ile Leu Ala Arg Ser Pro Lys Pro Leu Asp Lys Glu Leu Lys Lys
210 215 220
Lys Ile Ala Leu Ser Cys Asp Val Glu Gln Asp Ser Val Ile Val Ala
225 230 235 240
Thr Asp Thr Lys Ser Ile Tyr Ala Cys Pro Ile Leu Phe Leu Gln Glu
245 250 255
Gly Ile Leu Thr Pro Ile Ala Arg Arg Phe Asn Leu Asn Lys Leu His
260 265 270
Pro Lys Met Ala Ala Trp Asn Thr Leu Val Glu Lys Ile Ile Ala Pro
275 280 285
Lys His Lys Val Lys Ile Gly Phe Val Gly Lys Tyr Leu Ser Leu Lys
290 295 300
Glu Ser Tyr Lys Ser Leu Ile Glu Ala Leu Ile His Ala Gly Ala His
305 310 315 320
Leu Asp Thr Gln Val Asn Ile Glu Trp Leu Asp Ser Glu Asn Phe Asn
325 330 335
Glu Lys Thr Asp Leu Glu Gly Val Asp Ala Ile Leu Val Pro Gly Gly
340 345 350
Phe Gly Glu Arg Gly Ile Glu Gly Lys Ile Cys Ala Ile Gln Arg Ala
355 360 365
Arg Leu Glu Lys Leu Pro Phe Leu Gly Ile Cys Leu Gly Met Gln Leu
370 375 380
Ala Ile Val Glu Phe Cys Arg Asn Val Leu Gly Leu Lys Gly Ala Asn
385 390 395 400
Ser Thr Glu Phe Asn Gln Arg Cys Glu Tyr Pro Val Val Tyr Leu Ile
405 410 415
Glu Asp Phe Met Asp Gln Asn His Gln Lys Gln Val Arg Thr Tyr Asn
420 425 430
Ser Pro Leu Gly Gly Thr Met Arg Leu Gly Glu Tyr Glu Cys Glu Ile
435 440 445
Met Pro Asn Ser Leu Leu Glu Lys Ala Tyr Lys Lys Pro Asn Ile Lys
450 455 460
Glu Arg His Arg His Arg Tyr Glu Ile Asn Pro Lys Tyr Arg Gln Glu
465 470 475 480
Trp Glu Asn Lys Gly Leu Lys Val Val Gly Phe Gly Ala Asn His Leu
485 490 495
Ile Glu Ala Ile Glu Leu Glu Asp His Pro Phe Phe Val Gly Val Gln
500 505 510
Phe His Pro Glu Phe Thr Ser Arg Leu Gln Ser Pro Asn Pro Ile Ile
515 520 525
Leu Asp Phe Ile Lys Ser Ala Leu His Lys Ser
530 535

```

(2) INFORMATION FOR SEQ ID NO:1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1643

SUBSTITUTE SHEET (RULE 26)

1188

```

      50              55              60
Val Asp Ile Trp Val Tyr Ser Asp Val Arg Gln Phe Leu Leu Asp Thr
65              70              75              80
Ser Ser Ser Phe Ile Trp Leu Leu Ile Ala Leu Leu Ile Lys Trp Gly
      85              90              95
Val Ile Val Ile Ser Ala Arg Lys Cys Tyr Gln Phe Ser Gln Lys Met
      100              105              110
Phe Ala Leu Ile Gln Arg Lys Arg Gln Ile Arg Glu Asn Leu Lys Asn
      115              120              125
Arg Ser Asn Arg Lys Asp Ala Lys Asn Phe Glu Lys Leu Ser Asn Ile
      130              135              140
Ala Glu Glu Ile Ile Ser Lys Lys Gln Glu Glu Ser His His Lys Glu
145              150              155              160
Asp Ser Asn Asp Glu Asn His Lys Asp Lys Leu Ser Asn Ile Thr Glu
      165              170              175
Glu Met Ile Leu Lys Lys Gln Glu Glu Leu Lys Ala Arg Lys Asp Lys
      180              185              190
Gly Asp

```

(2) INFORMATION FOR SEQ ID NO:1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1642

```

Leu Met Asp Arg Ala Lys Phe Ile Phe Val Thr Gly Gly Val Leu Ser
1              5              10              15
Ser Leu Gly Lys Gly Ile Ser Ser Ser Ile Ala Thr Leu Leu Gln
      20              25              30
His Cys Asn Tyr Gln Val Ser Ile Leu Lys Ile Asp Pro Tyr Ile Asn
      35              40              45
Ile Asp Pro Gly Thr Met Ser Pro Leu Glu His Gly Glu Val Phe Val
      50              55              60
Thr Ser Asp Gly Ala Glu Thr Asp Leu Asp Ile Gly His Tyr Glu Arg
65              70              75              80
Phe Leu Asn Arg Asn Leu Thr Arg Leu Asn Asn Phe Thr Thr Gly Gln
      85              90              95
Ile Phe Ser Ser Val Ile Glu Asn Glu Arg Lys Gly Glu Tyr Leu Gly
      100              105              110
Lys Thr Ile Gln Ile Val Pro His Val Thr Asp Glu Ile Lys Arg Arg
      115              120              125
Ile Lys Ser Ala Ala Lys Gly Leu Asp Phe Leu Ile Val Glu Val Gly
      130              135              140
Gly Thr Val Gly Asp Met Glu Gly Met Phe Tyr Val Glu Pro Ile Arg
145              150              155              160
Gln Leu Lys Leu Glu Leu Arg Asn Lys Ala Leu Ile Asn Met His Val
      165              170              175
Thr Leu Met Pro Tyr Ile Arg Ala Thr Ser Glu Leu Arg Ser Arg Pro
      180              185              190

```

SUBSTITUTE SHEET (RULE 26)

1187

```

Arg Leu Lys Met Ala Thr Lys Leu Thr Pro Lys Gln Lys Ala Gln Leu
1      5      10      15
Asp Glu Leu Ser Ser Met Ser Glu Lys Ile Ala Ile Leu Leu Ile Gln Val
20      25      30
Gly Glu Asp Thr Thr Gly Glu Ile Leu Arg His Leu Asp Ile Asp Ser
35      40      45
Ile Thr Glu Ile Ser Lys Gln Ile Val Gln Leu Asn Gly Thr Asp Lys
50      55      60
Gln Ile Gly Ala Ala Val Leu Glu Glu Phe Phe Ala Ile Phe Gln Ser
65      70      75      80
Asn Gln Tyr Ile Asn Thr Gly Gly Leu Glu Tyr Ala Arg Glu Leu Leu
85      90      95
Thr Arg Thr Leu Gly Ser Glu Glu Ala Arg Lys Val Met Asp Lys Leu
100     105     110
Thr Lys Ser Leu Gln Thr Gln Lys Asn Phe Ala Tyr Leu Gly Lys Ile
115     120     125
Lys Pro Gln Gln Leu Ala Asp Phe Ile Ile Asn Glu His Pro Gln Thr
130     135     140
Ile Ala Leu Ile Leu Ala His Met Glu Ala Pro Asn Ala Ala Glu Thr
145     150     155     160
Leu Ser Tyr Phe Pro Asp Glu Met Lys Ala Glu Ile Ser Ile Arg Met
165     170     175
Ala Asn Leu Gly Glu Ile Ser Pro Gln Val Val Lys Arg Val Ser Thr
180     185     190
Val Leu Glu Asn Lys Leu Glu Ser Leu Thr Ser Tyr Lys Ile Glu Val
195     200     205
Gly Gly Leu Arg Ala Val Ala Glu Ile Phe Asn Arg Leu Gly Gln Lys
210     215     220
Ser Ala Lys Thr Thr Leu Ala Arg Ile Glu Ser Val Asp Asn Lys Leu
225     230     235     240
Ala Gly Ala Ile Lys Glu Met Met Phe Thr Phe Glu Asp Ile Ala Lys
245     250     255
Leu Asp Asn Phe Ala Ile Met Arg Asp Phe Lys Ser Gly Gly Leu Lys
260     265     270
Lys Thr Gly Leu
275

```

(2) INFORMATION FOR SEQ ID NO:1641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1641

```

Arg Ser Leu Gly Lys Gly Arg Pro Met Asn Lys Lys Asn Ser Val Ile
1      5      10      15
Ser Gly Leu Met Asn Phe Phe Ser Glu Lys Asn Glu Arg Trp Leu Leu
20      25      30
Ala His Arg His Thr Arg Gly Phe Val Ile Val Ala Trp Leu Phe Arg
35      40      45
Phe Lys Ser Ile Ala Phe Ser Ile Leu Ile Thr Leu Leu Val Ile Leu

```

SUBSTITUTE SHEET (RULE 26)

1186

(A) LENGTH: 199 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1639

```

Lys Trp Cys Gly Tyr Cys Glu Arg Arg Ser Val Arg Arg Gly Tyr Tyr
1      5      10      15
Arg Ser Arg Lys Arg Leu Thr Lys Asn His His Ala Phe Ala Cys Ser
20     25     30
Leu Asp Phe Ile Tyr Pro Thr Asn Asn His Lys Val Ile Gln Glu Ile
35     40     45
Ala Gln Asn Gly Leu Ile Leu Ser Glu His Glu Lys Asp Phe Met Phe
50     55     60
Ile Lys Gly Phe Phe Leu Val Arg Asn Cys Leu Val Ile Ala Leu Thr
65     70     75     80
Asp Ala Val Ile Ile Pro Gln Ala Asp Leu Lys Ser Gly Ser Met Ser
85     90     95
Ser Val Arg Leu Ala Gln Lys Tyr Gln Lys Pro Leu Phe Val Leu Pro
100    105    110
Gln Arg Leu Asn Glu Ser Asp Gly Thr Asn Glu Leu Leu Glu Lys Gly
115    120    125
Gln Ala Gln Gly Ile Phe Asn Ile Gln Asn Phe Ile Asn Thr Leu Leu
130    135    140
Lys Asp Tyr His Leu Lys Glu Met Pro Glu Met Lys Asp Glu Phe Leu
145    150    155    160
Glu Tyr Cys Ala Lys Asn Pro Ser Tyr Glu Glu Ala Tyr Leu Lys Phe
165    170    175
Gly Asp Lys Leu Leu Glu Tyr Glu Leu Leu Gly Lys Ile Lys Arg Ile
180    185    190
Asn His Leu Val Val Leu Ala
195

```

(2) INFORMATION FOR SEQ ID NO:1640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1640

1185

Ala Ser Gln Gly Ile Pro Lys Thr Ser Lys Val Gly Phe Glu Ile Phe
 115 120 125
 Asp Thr Lys Asp Phe Gly Ala Thr Asp Phe Asp Gln Asn Ile Lys Leu
 130 135 140
 Ile Arg Ala Ile Glu Gly Leu Ser Arg Thr Ile Glu Ser Leu Asn
 145 150 155 160
 Pro Ile Leu Lys Ala Asn Val His Ile Ala Ile Pro Lys Asp Ser Val
 165 170 175
 Phe Val Ala Lys Glu Val Pro Pro Ser Ala Ser Val Met Leu Lys Leu
 180 185 190
 Lys Pro Asp Met Lys Leu Ser Pro Thr Gln Ile Leu Gly Ile Lys Asn
 195 200 205
 Leu Ile Ala Ala Ala Val Pro Lys Leu Thr Ile Glu Asn Val Lys Ile
 210 215 220
 Val Asn Glu Asn Gly Glu Ser Ile Gly Glu Gly Asp Ile Leu Glu Asn
 225 230 235 240
 Ser Lys Glu Leu Ala Leu Glu Gln Leu Arg Tyr Lys Gln Asn Phe Glu
 245 250 255
 Asn Ile Leu Glu Asn Lys Ile Val Asn Ile Leu Ala Pro Ile Val Gly
 260 265 270
 Gly Lys Asn Lys Val Val Ala Arg Val Asn Ala Glu Phe Asp Phe Ser
 275 280 285
 Gln Lys Lys Ser Thr Lys Glu Thr Phe Asp Pro Asn Asn Val Val Arg
 290 295 300
 Ser Glu Gln Asn Leu Glu Lys Lys Glu Gly Ala Pro Lys Lys Gln
 305 310 315 320
 Val Gly Gly Val Pro Gly Val Val Ser Asn Ile Gly Pro Val Gln Gly
 325 330 335
 Leu Lys Asp Asn Lys Glu Pro Glu Lys Tyr Glu Lys Ser Gln Asn Thr
 340 345 350
 Thr Asn Tyr Glu Val Gly Lys Thr Ile Ile Glu Ile Lys Gly Glu Phe
 355 360 365
 Gly Thr Leu Met Arg Leu Asn Ala Ala Val Val Val Asp Gly Lys Tyr
 370 375 380
 Lys Ile Ala Leu Glu Asp Gly Ala Asn Ala Leu Glu Tyr Glu Pro Leu
 385 390 395 400
 Ser Asp Glu Ser Leu Lys Lys Ile Asn Ala Leu Val Lys Gln Ala Ile
 405 410 415
 Gly Asp Asn Gln Asn Arg Gly Asp Asp Val Ala Val Ser Asn Phe Glu
 420 425 430
 Phe Asn Pro Met Ala Pro Met Ile Asp Asn Ala Thr Leu Ser Glu Lys
 435 440 445
 Ile Met His Lys Thr Gln Lys Ile Leu Gly Ser Phe Thr Pro Leu Ile
 450 455 460
 Lys Tyr Ile Leu Val Phe Ile Val Leu Phe Ile Phe Tyr Lys Lys Val
 465 470 475 480
 Ile Val Pro Phe Ser Glu Arg Met Leu Glu Val Val Pro Asp Glu Asp
 485 490 495
 Lys Glu Val Lys Ser Met Phe Glu Glu Met Asp Glu Glu Glu Asp Glu
 500 505 510
 Leu Asn Lys Leu Gly Asp Leu Arg Lys Lys Val Glu Asp Gln Leu Gly
 515 520 525
 Leu Asn Ala Ser Phe Ser Glu Glu Val Arg Tyr Glu Ile Ile Leu
 530 535 540
 Glu Lys Ile Arg Gly Thr Leu Lys Glu Arg Pro Asp Glu Ile Ala Thr
 545 550 555 560
 Leu Phe Lys Leu Leu Ile Lys Asp Glu Ile Ser Ser Asp Ser Ala Lys
 565 570 575
 Gly

(2) INFORMATION FOR SEQ ID NO:1639:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

1343

```

Leu Asn Ser Glu His Pro Leu Phe Asp Trp Ala Ser Lys Gln Thr Tyr
1      5      10      15
Ile Gln Met Ala Asn Met Met Met Ala Ala Met Leu Gly Ile Asp
      20      25      30
Ser Cys Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Ala Ala Tyr Leu
      35      40      45
Glu Glu Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met
50      55      60
Ala Ser Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp
65      70      75      80
Lys Thr Glu Val Ile Tyr Glu Val Ile Glu
      85      90

```

(2) INFORMATION FOR SEQ ID NO:1815:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1815

```

Lys Glu Ile Thr Met Arg Lys Leu Phe Ile Pro Leu Leu Leu Phe Ser
1      5      10      15
Ala Leu Glu Ala Asn Glu Lys Asn Gly Phe Phe Ile Glu Ala Gly Phe
      20      25      30
Glu Thr Gly Leu Leu Glu Gly Thr Gln Thr Gln Glu Lys Arg His Thr
35      40      45
Thr Thr Lys Asn Thr Tyr Ala Thr Tyr Asn Tyr Leu Pro Thr Asp Thr
50      55      60
Ile Leu Lys Arg Ala Ala Asn Leu Phe Thr Asn Ala Glu Ala Ile Ser
65      70      75      80
Lys Leu Lys Phe Ser Ser Leu Ser Pro Val Arg Val Leu Tyr Met Tyr
85      90      95
Asn Gly Gln Leu Thr Ile Glu Asn Phe Leu Pro Tyr Asn Leu Asn Asn
100      105      110
Val Lys Leu Ser Phe Thr Asp Ala Gln Gly Asn Val Ile Asp Leu Gly
115      120      125
Val Ile Glu Thr Ile Pro Lys His Ser Lys Ile Val Leu Pro Gly Glu
130      135      140
Ala Phe Asp Ser Leu Lys Ile Asp Pro Tyr Thr Leu Phe Leu Pro Lys
145      150      155      160
Ile Glu Ala Thr Ser Thr Ser Ile Ser Asp Ala Asn Thr Gln Arg Val
165      170      175
Phe Glu Thr Leu Asn Lys Ile Lys Thr Asn Leu Val Val Asn Tyr Arg
180      185      190
Asn Glu Asn Lys Phe Lys Asp His Glu Asn His Trp Glu Ala Phe Thr
195      200      205
Pro Gln Thr Ala Glu Glu Phe Thr Asn Leu Met Leu Asn Met Ile Ala
210      215      220
Val Leu Asp Ser Gln Ser Trp Gly Asp Ala Ile Leu Asn Ala Pro Phe
225      230      235      240
Glu Phe Thr Asn Ser Pro Thr Asp Cys Asp Asn Asp Pro Ser Lys Cys

```

SUBSTITUTE SHEET (RULE 26)

1344

```

                245                250                255
Val Asn Pro Gly Thr Asn Gly Leu Val Asn Ser Lys Val Asp Gln Lys
                260                265                270
Tyr Val Leu Asn Lys Gln Asp Ile Val Asn Lys Phe Lys Asn Lys Ala
                275                280                285
Asp Leu Asp Val Ile Val Leu Lys Asp Ser Gly Val Val Gly Leu Gly
                290                295                300
Ser Asp Ile Thr Pro Ser Asn Asn Asp Asp Gly Lys His Tyr Gly Gln
                305                310                315                320
Leu Gly Val Val Ala Ser Ala Leu Asp Pro Lys Lys Leu Phe Gly Asn
                325                330                335
Asp Leu Lys Thr Ile Asn Leu Glu Asp Leu Arg Thr Ile Leu His Glu
                340                345                350
Phe Ser His Thr Lys Gly Tyr Gly His Asn Gly Asn Met Thr Tyr Gln
                355                360                365
Arg Val Pro Val Thr Lys Asp Val Lys
                370                375

```

(2) INFORMATION FOR SEQ ID NO:1816:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1816

```

Ile Met Gly Val Gly Glu Lys Glu Glu Lys Lys Glu Ser Gln Lys Val
1      5      10      15
Ala Val Ile Thr Gly Ala Ser Ser Gly Ile Gly Leu Glu Cys Val Leu
      20      25      30
Met Leu Leu Asn Gln Gly Tyr Lys Val Tyr Ala Leu Ser Arg His Ala
      35      40      45
Thr Leu Cys Val Ala Leu Asn His Ala Leu Cys Glu Cys Val Asp Ile
      50      55      60
Asp Val Ser Asp Ser Asn Ala Leu Lys Glu Val Phe Leu Asn Ile Ser
      65      70      75      80
Ala Lys Glu Asp His Cys Asp Val Leu Ile Asn Ser Ala Gly Tyr Gly
      85      90      95
Val Phe Gly Ser Val Glu Asp Thr Pro Ile Glu Glu Val Lys Lys Gln
      100     105     110
Phe Ser Val Asn Phe Phe Ala Leu Cys Glu Val Val Gln Leu Cys Leu
      115     120     125
Pro Leu Leu Lys Asn Lys Pro Tyr Ser Lys Ile Phe Asn Leu Ser Ser
      130     135     140
Ile Ala Gly Arg Val Ser Met Leu Phe Leu Gly His Tyr Ser Ala Ser
      145     150     155     160
Lys His Ala Leu Glu Ala Tyr Ser Asp Ala Leu Arg Leu Glu Leu Lys
      165     170     175
Pro Phe Asn Val Gln Val Cys Leu Ile Glu Pro Gly Pro Val Lys Ser
      180     185     190
Asn Trp Glu Lys Thr Ala Phe Glu Asn Asp Glu Arg Lys Asp Ser Val
      195     200     205

```

SUBSTITUTE SHEET (RULE 26)

1345

Tyr Ala Leu Glu Val Asn Ala Ala
210 215

(2) INFORMATION FOR SEQ ID NO:1817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...256

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1817

```

Asp Ser Asn Arg Ser Ala Phe Ile Cys His Asn Leu Ala Met Val Leu
1      5      10      15
Met Ile Phe Thr Ser Ile Leu Lys Ile Ala Leu Lys Val Leu Ser Glu
20      25      30
Arg Lys Lys Asn Arg Tyr Gly Phe Pro Arg Ile Phe Asp Val Ala Asp
35      40      45
Ile Glu Gln Glu Glu Arg Glu Val Ile Glu Trp Arg Glu Lys Lys Lys
50      55      60
Ala Ser Lys Gln Ser Tyr Lys Lys Gln Asn Leu Gln Ile Asn Lys Ile Ala
65      70      75      80
Asn Asp Leu Lys Arg Asp Lys Ile Val Asp Lys Arg Thr Ile Leu Ser
85      90      95
Val Ile Asp Ala Asp Ile Glu Arg Gly Phe Ile Pro Pro Lys Asp Leu
100     105     110
Leu Lys Gln Leu Glu Lys Ile Ser Ala Ser Leu Ser Lys Asp Ile Val
115     120     125
Ile Thr Ile Lys Gln Val Glu Lys Leu Glu Leu Asn Tyr Ala Leu Ile
130     135     140
Asp Asn Ile Gln His Asn Thr Leu Asp Asp Thr Leu Asp Phe Thr Phe
145     150     155     160
Ile Val Gly Asp Ser Leu Ser Val Gln Ser Leu Tyr Val Thr Phe Asn
165     170     175
Leu Val Ile Asp Ile Asp Arg Pro Met Ser Glu Gln Phe Leu Asn His
180     185     190
Ile Gly Lys Leu Gly Ser Phe Glu Ser Arg Glu Gln Ala Leu Glu Trp
195     200     205
Val Arg Leu Ser Gln Thr Lys Leu Ile Ile Glu Thr Pro Lys Glu Ala
210     215     220
Leu Lys Asn Ala Glu Leu Ser Gln Ile Glu Glu Ile Leu Thr Gly Cys
225     230     235     240
Ile Phe Asn Gly Ala Tyr Arg Leu Gln Asn Asp Leu Lys Lys Gly Arg
245     250     255

```

(2) INFORMATION FOR SEQ ID NO:1818:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

1346

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1818

```

Gly Asn Ala Arg Thr Cys Ile Val Ile Cys Trp Asp Cys Leu Asn Gln
1      5      10      15
Gln Trp Asp Cys Gly Leu Thr Lys Val Asp Pro Lys Ser Thr Ala Val
20     25     30
Met Asn Phe Phe Val Gly Gly Leu Ser Ile Val Cys Asn Val Val Val
35     40     45
Ile Thr Tyr Ser Ala Leu His Pro Thr Ala Pro Val Glu Gly Ala Glu
50     55     60
Asp Ile Val Gln Val Ser His His Leu Thr Ser Phe Tyr Gly Pro Ala
65     70     75     80
Thr Gly Leu Leu Phe Gly Phe Thr Tyr Leu Tyr Ala Ala Ile Asn His
85     90     95
Thr Phe Gly Leu Asp Trp Arg Pro Tyr Ser Trp Tyr Ser Leu Phe Val
100    105    110
Ala Ile Asn Thr Val Pro Ala Ala Ile Leu Ser His Tyr Ser Asp Met
115    120    125
Leu Asp Asp His Lys Val Leu Gly Ile Thr Glu Gly Asp Trp Trp Ala
130    135    140
Ile Ile Trp Leu Ala Trp Gly Val Leu Trp Leu Thr Ala Phe Ile Glu
145    150    155    160
Asn Ile Leu Lys Ile Pro Leu Gly Lys Phe Thr Pro Trp Leu Ala Ile
165    170    175
Ile Glu Gly Ile Leu Thr Ala Trp Ile Pro Ala Trp Leu Leu Phe Ile
180    185    190
Gln His Trp Val
195

```

(2) INFORMATION FOR SEQ ID NO:1819:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 640 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1819

```

Ser Ile Cys His Glu Tyr Leu Lys Val Asn Leu Gln Glu Lys Leu Ala
1      5      10      15
Gly Phe Arg Asp Phe Val His Tyr Asn Glu Asn Ala Lys Asp Ser Leu
20     25     30

```

SUBSTITUTE SHEET (RULE 26)

1347

Pro Leu Lys Ala Leu Phe Leu Ser Gly Val Asp Ala Leu Ser Lys Asp
 35 40 45
 Ala Leu Tyr Tyr Leu Glu Lys Ile Met Arg Phe Gly Ser Lys Asn Gly
 50 55 60
 Val Leu Ser Phe Val Asn Leu Glu Ser Glu Lys Asn Asn Gln Ser Ala
 65 70 75 80
 Glu Asp Leu Lys Arg Tyr Ala Glu Phe Phe Lys Asp Arg Thr Ser Phe
 85 90 95
 Glu Gly Leu Lys Tyr Leu Asn Val Glu Ile Ile Ser Asp Gln Gly Ile
 100 105 110
 Lys Ser Gln His Met Gln Asp Phe Ala Asp Lys Ile Lys Ala Tyr Tyr
 115 120 125
 Lys Gln Lys Lys Glu Val Lys Arg Glu Leu Lys Asp Leu Gln Arg Asp
 130 135 140
 Lys Glu Phe Trp Thr Lys Ser Ser Gln His Glu Val Ser Val Pro Val
 145 150 155 160
 Gly Trp Asp Ile Asn His Lys Glu Val Cys Phe Lys Ile Gly Asn Glu
 165 170 175
 Gln Asn His Thr Leu Ile Cys Asp His Ser Gly Ser Gly Lys Ser Asn
 180 185 190
 Phe Leu His Val Leu Ile Gln Asn Leu Ala Phe Tyr Tyr Asp Pro Asp
 195 200 205
 Glu Val Gln Leu Phe Leu Leu Asp Tyr Lys Glu Gly Val Glu Phe Asn
 210 215 220
 Ala Tyr Val Ala Asp Pro Ala Leu Glu His Ala Arg Leu Val Ser Val
 225 230 235 240
 Ala Ser Ser Ile Ser Tyr Gly Ile Thr Phe Leu Lys Trp Leu Cys Asp
 245 250 255
 Glu Met Gln Lys Arg Ala Asp Arg Phe Lys Gln Phe Asn Val Lys Asp
 260 265 270
 Leu Ser Asp Tyr Arg Lys His Glu Lys Met Pro Arg Leu Ile Val Val
 275 280 285
 Ile Asp Glu Phe Gln Val Leu Phe Ser Asp Asn Lys Ser Thr Lys Ala
 290 295 300
 Val Glu Gly His Leu Asn Thr Leu Leu Lys Lys Gly Arg Ser Tyr Gly
 305 310 315 320
 Val His Leu Val Leu Ala Thr Gln Thr Met Arg Gly Thr Asp Ile Asn
 325 330 335
 Pro Ser Phe Lys Ala Gln Ile Ala Asn Arg Ile Ala Leu Pro Met Asp
 340 345 350
 Ala Glu Asp Ser Ser Ser Val Leu Gly Asp Asp Ala Ala Cys Glu Ile
 355 360 365
 Gln Asn Pro Glu Gly Ile Phe Asn Asn Asn Gly Gly Asn Arg Lys Tyr
 370 375 380
 His Thr Lys Met Ser Val Pro Lys Ala Pro Asp Asp Phe Lys Ser Phe
 385 390 395 400
 Leu Thr Lys Ile His Ala Glu Phe Asn Gln Arg Asn Leu Ala Pro Ile
 405 410 415
 Asp Arg Lys Ile Tyr Asn Gly Glu Thr Pro Leu Lys Met Pro Asp Thr
 420 425 430
 Leu Lys Ala Asn Glu Met Arg Leu His Leu Gly Lys Lys Val Asp Tyr
 435 440 445
 Glu Gln Lys Asp Leu Ile Val Glu Phe Glu Ser Asn Glu Ser His Leu
 450 455 460
 Leu Val Val Ile Gln Asp Leu Asn Ala Arg Ile Ala Leu Met Lys Leu
 465 470 475 480
 Leu Phe Gln Asn Val Lys Ser Ala Asn Lys Glu Leu Val Phe Cys Asn
 485 490 495
 Lys Glu Lys Arg Leu Ile Arg Ser Phe Asp Ala Gln Lys Glu Tyr Gly
 500 505 510
 Ile Thr Pro Val Glu Asn Ile Leu Ser Val Leu Asp Thr Ala Met Asn
 515 520 525
 Pro Asn Ser Ala Leu Val Ile Asp Asn Leu Asn Glu Ala Lys Glu Leu
 530 535 540
 His Asp Lys Val Gly Ala Glu Lys Leu Lys Ser Phe Leu Glu Lys Ala

1348

```

545          550          555          560
Ile Asp Asn Glu Gln Tyr Cys Val Ile Phe Ala His Asp Phe Arg Gln
          565          570          575
Ile Lys Thr Asn Tyr His Phe Asp Lys Leu Lys Glu Leu Leu Asn Asn
          580          585          590
His Phe Lys Glu Cys Leu Ala Phe Arg Cys Asn Gly Glu Asn Leu Asn
          595          600          605
Ala Ile Lys Ser Asp Leu Pro Pro Pro Ser Lys Leu Asn Val Leu Leu
          610          615          620
Ile Glu Leu Ser Lys Asp Ser Val Thr Glu Phe Arg Pro Phe Ser Leu
625          630          635          640

```

(2) INFORMATION FOR SEQ ID NO:1820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1820

```

Arg Pro Asn Leu Ser Ser Gln Phe Leu Tyr Thr Glu Met Leu Ser Leu
1          5          10          15
Lys Leu Thr Tyr Glu Ser Thr Leu Gln Gln Asp Leu Lys Lys Ile Leu
          20          25          30
Gly Ile Glu Glu Val Ile Met Leu Ser Thr Ser Pro Met Glu Leu Arg
          35          40          45
Leu Ala Asn Gln Lys Leu Gly Asn Arg Phe Ile Lys Thr Leu Gln Ala
          50          55          60
Met Asn Glu Leu Asp Met Gly Ala Phe Phe Asn Ala Tyr Ala Gln Thr
65          70          75          80
Thr Gln Arg Ser His Pro Cys His
          85

```

(2) INFORMATION FOR SEQ ID NO:1821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...223

1349

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1821

```

Glu Lys Ser Thr Ser Asn Leu Lys Lys Pro Ser Val Trp Arg Ser Lys
1      5      10      15
Leu Ile Cys Lys Ile Ala Thr His Lys Ala Arg Ser Ile Gly Leu Cys
20     25     30
Val Lys Pro Lys Ser Met Lys Glu Lys Leu Arg Gly Ala Met Val Asn
35     40     45
Ile Leu Arg Ile Lys Met Ile Glu Ile Ser Glu Trp Leu Gln Lys Leu
50     55     60
Asp Asp Ala Leu Asp Lys Val Val Ala Lys Lys Glu Pro Glu Ser Phe
65     70     75     80
Leu Lys Pro Ile Ile Ser Pro Ile Glu Asp Tyr Gln Lys Ser Val Arg
85     90     95
Gln Ile Gln Ala Gln Phe Thr Asp Ala Pro Lys Phe Asn Glu Glu Gly
100    105    110
Ala Tyr Pro Gln Phe Leu Ser Cys Gly Leu Leu Gln Val Arg Gly Lys
115    120    125
Asn Gly Ala Asn Met Glu Phe Leu Leu Pro Lys Val Tyr Pro Phe Pro
130    135    140
Pro Lys Ser Leu Tyr Ile Glu His Glu Lys Asp Gly Gln Phe Leu Arg
145    150    155    160
Glu Met Leu Met Arg Leu Leu Ser Ser Ala Pro Leu Val Gln Leu Glu
165    170    175
Val Ile Leu Ile Asp Ala Leu Ser Leu Gly Gly Ile Phe Asn Leu Ala
180    185    190
Arg Arg Leu Leu Asp Lys Asn Asn Asp Phe Ile Tyr Gln Gln Arg Ile
195    200    205
Leu Thr Glu Ser Lys Glu Ile Glu Glu Ala Leu Lys His Leu Pro
210    215    220

```

(2) INFORMATION FOR SEQ ID NO:1822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1822

```

Thr Trp Val His Phe Leu Thr Leu Thr Leu Lys Gln Pro Lys Asp Pro
1      5      10      15
Thr His Ala Thr Ser Tyr Gly Val Phe Ala Ala Ser Leu Asn Met Glu
20     25     30
Leu Lys Lys Ala Leu Arg His Tyr Leu Tyr Ala Gln Thr Ser Asn Met
35     40     45
Val Ile Asn Cys Val Lys Ser Val Pro Leu Ser Gln Asn Asp Gly Gln
50     55     60
Lys Ile Leu Leu Ser Leu Gln Ser Pro Phe Asn Gln Leu Ile Glu Lys
65     70     75     80
Thr Leu Glu Leu Asp Glu Ser His Leu Cys Ala Ala Ser Val Gln Asn
85     90     95
Asp Ile Lys Ala Met Gln His Glu Ser Leu Tyr Ser Arg Leu Tyr Met

```

1350

Ser 100 105 110

(2) INFORMATION FOR SEQ ID NO:1823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1823

```

Arg Ala Ser Met Lys Asn Phe Ser Pro Leu Tyr Cys Leu Lys Lys Leu
1           5           10           15
Lys Lys Arg His Leu Ile Ala Leu Ser Leu Pro Leu Leu Ser Tyr Ala
20           25           30
Asn Gly Phe Lys Ile Gln Glu Gln Ser Leu Asn Gly Thr Ala Leu Gly
35           40           45
Ser Ala Tyr Val Ala Gly Ala Arg Gly Ala Asp Ala Ser Phe Tyr Asn
50           55           60
Pro Ala Asn Met Gly Phe Thr Asn Asp Trp Gly Glu Asn Arg Ser Glu
65           70           75           80
Phe Glu Met Thr Thr Thr Val Ile Asn Ile Pro Ala Phe Ser Phe Lys
85           90           95
Val Pro Thr Thr Asn Gln Gly Leu Tyr Ser Val Thr Ser Leu Glu Ile
100          105          110
Asp Lys Ser Gln Gln Asn Ile Leu Gly Ile Ile Asn Thr Ile Gly Leu
115          120          125
Gly Asn Ile Leu Lys Ala Leu Gly Asn Thr Ala Ala Thr Asn Gly Leu
130          135          140
Ser Gln Gly Ile Asn Arg Val Gln Gly Val Met Asn
145          150          155

```

(2) INFORMATION FOR SEQ ID NO:1824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...217

1351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1824

```

Ala Asp Arg Glu Asp Lys Leu Ser His Ser Ile Ile Met Arg Tyr Phe
1      5      10      15
Arg Ser Ala Phe Leu Leu Phe Phe Met Thr Leu Phe Phe Val Ser Cys
      20      25      30
Ser Lys His Pro Phe Ser Lys Gln Thr Pro Lys Thr Lys Glu Arg Ile
      35      40      45
Arg Gln Glu Glu Ala Asn Lys Lys Arg Glu Glu Thr Leu Asn Ala Leu
      50      55      60
Arg Gln Phe Arg Leu Ile Tyr Ile Asn Thr Pro Val Phe Arg Phe Tyr
65      70      75      80
Asp Tyr Gly Thr Ile Lys Thr Asp Lys Asp His Asn Thr Glu Val Thr
      85      90      95
Leu Tyr Lys Leu Ser Gln Lys Val Gly Asp Ile Tyr Met Thr Lys Arg
      100      105      110
Ser Ile Cys Phe Ser Gln Lys Cys Ser Ala Lys Trp Ile Ala Ala Arg
      115      120      125
Asp Leu Phe Gly Lys Val Ser Tyr Gly Asp Leu Phe Asp Asp Ile Val
130      135      140
Leu Gly Arg Asp Ile Phe Lys Gly Leu Gly Lys Arg His Leu Thr Pro
145      150      155      160
Glu Tyr Val Ile Gln Arg Phe Gln Lys Ser Gly Glu Ile Ile Leu Tyr
      165      170      175
Glu Arg Lys Asn Gly Leu Ile Ser Phe Gln Asn Leu Thr Gln Lys Ile
      180      185      190
Ala Ile Arg Ile Glu Pro Tyr Glu Pro Ser Leu Gln Asp Leu Glu Asp
      195      200      205
Asn Glu Asn Ala Asp Ser Glu Leu Gln
210      215

```

(2) INFORMATION FOR SEQ ID NO:1825:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1825

```

Glu Ile Ala Glu Ile Val Ser Gln Trp Thr His Ile Pro Phe Gln Lys
1      5      10      15
Met Phe Gln Ser Glu Lys Asn Arg Val Leu Asn Ile Glu Ser Glu Leu
      20      25      30
Gln Lys Arg Val Val Gly Gln Glu Lys Ala Leu Lys Ala Ile Ala Lys
      35      40      45
Ala Ile Lys Arg Asn Lys Ala Gly Leu Ser Asp Ser Asn Lys Pro Ile
      50      55      60
Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Glu Ser
65      70      75      80
Ala Lys Ala Leu Ala Gln Phe Leu Phe Asp Ser Asp Lys Asn Leu Ile
      85      90      95
Arg Ile Asp Met Ser Glu Tyr Met Glu Lys His Ala Ile Ser Arg Leu

```

1352

```

      100      105      110
Ile Gly Ala Ala Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu
      115      120      125
Thr Glu Ala Val Arg Arg Lys Pro Tyr Ser Val Val Leu Leu Asp Glu
      130      135      140
Val Glu Lys Ala His Pro Asp Val Phe Asn Phe Leu Leu Gln Val Phe
      145      150      155      160
Asp Glu Gly His Leu Thr Asp Ser Lys Gly Val Arg Val Asp Phe Lys
      165      170      175
Asn Thr Ile Leu Ile Leu Thr Ser Asn Val Ala Ser Gly Ala Leu Leu
      180      185      190
Glu Glu Asp Leu Ser Glu Ala Asp Lys Gln Lys Ala Ile Lys Glu Ser
      195      200      205
Leu Arg Gln Phe Phe Lys Pro Glu Phe Leu Asn Arg Leu Asp Glu Ile
      210      215      220
Ile Ser Phe Asn Ala Leu Asp Ser His Ala Ile Ile
      225      230      235

```

(2) INFORMATION FOR SEQ ID NO:1826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1826

```

Val Arg Phe Cys Tyr Ser Lys Lys Tyr Lys Lys Thr Ile Ile Leu Lys
1      5      10      15
Lys Asp Trp Met Met Phe Asp Asn Thr Leu Ile Asn Leu Phe Glu Thr
      20      25      30
Ala Pro Leu Leu Thr Ser Leu Leu Ala Gly Ile Leu Thr Phe Leu Ser
      35      40      45
Pro Cys Val Leu Pro Leu Ile Pro Ala Tyr Met Ser Tyr Ile Ser Gln
      50      55      60
Ile Ser Leu Glu Asp Ile Lys Asp Gly Lys Ala Lys Arg Val Ser Val
      65      70      75      80
Phe Leu Lys Ser Leu Met Phe Val Val Gly Phe Ser Leu Val Phe Leu
      85      90      95
Gly Val Gly Met Ser Met Ala Lys Leu Ile His Ser Phe Ser Phe Ser
      100      105      110
Trp Val Asn Tyr Ile Ala Gly Gly Ile Val Ile Leu Phe Gly Leu His
      115      120      125
Phe Leu Gly Val Phe Arg Phe Ala Leu Leu Tyr Lys Thr Gln Ser Ala
      130      135      140
Gly Leu Ala Ser Lys Ser Asn Ser Met Gln Arg Phe Tyr Pro Phe Leu
      145      150      155      160
Leu Gly Met Ser Phe Ala Leu Gly Trp Thr Pro Cys Ile Gly Pro Ile
      165      170      175
Phe Thr Ser Ile Val Ile Met Ser Ala Ser Lys Asp Ala Tyr Gly Leu
      180      185      190
Met Leu Met Val Val Phe Val Met Gly Leu Ala Ile Pro Phe Val Leu
      195      200      205

```

SUBSTITUTE SHEET (RULE 26)

1353

Val Ala Leu Met Leu Glu Arg Ala Leu Leu Phe Leu Lys Ser Leu Arg
 210 215 220
 Lys Tyr Asn Arg Ala Ile Glu Ile Val Ser Gly Leu Val Leu Ile Leu
 225 230 235 240
 Met Gly Ile Leu Ile Met Thr Asn Ser Leu Glu Ser Leu Thr Asn Phe
 245 250 255
 Leu Gln Asn

(2) INFORMATION FOR SEQ ID NO:1827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1827

Ile Gly Gly Ala His Ala Phe Leu Tyr Tyr Leu Thr Phe Leu Phe Ile
 1 5 10 15
 Val Gly Phe Gly Val Phe Val Tyr Ser Ile Asp Pro Gln Ala Tyr Ala
 20 25 30
 Phe Asn Leu Gly Ser Tyr Ser Phe Asn Leu Pro Ile Ala Val Trp Leu
 35 40 45
 Met Gly Val Leu Gly Met Phe Ala Phe Phe Ser Trp Val Phe Leu Phe
 50 55 60
 Lys His Asn Leu Ser His Lys Ile Arg Leu Tyr His Glu Lys Lys Asp
 65 70 75 80
 Phe Asp Lys Leu Leu Lys Gln Ile Leu Ser Gln Asp Thr Gln Lys Thr
 85 90 95
 Phe Leu Lys Thr Lys Phe Lys Ser Asp Leu Ala Lys Asn Leu Ser Gln
 100 105 110
 Ile Leu Ala Arg Tyr Asp Leu Lys Ala Asp Leu Asn Thr Pro Asn Ser
 115 120 125
 Gly Cys Glu Lys Val Asp Asn Leu Phe Lys His Tyr His Asn Ile Glu
 130 135 140
 Asn Asn Thr Leu Glu Pro Lys Asp His Ala Lys His Ser Leu Ala Tyr
 145 150 155 160
 Glu His Ala Tyr Phe Ser Lys Arg Leu Lys Ala Phe Ile His Asn Asp
 165 170 175
 Leu Lys Asn Ala Phe Glu Val Leu Thr Asn Ala Gln Ile Pro Leu Glu
 180 185 190
 Leu Arg Arg Tyr Ala Leu
 195

(2) INFORMATION FOR SEQ ID NO:1828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

1354

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1828

```

Gln Asp Lys Gly Leu Leu Leu Ser Val Ala Leu Pro Asn Ser Asn Asn
1      5      10      15
Ala Ser Gln Asn Asn Ile Leu Ser Leu Ser Val Leu His Asn Gln Ile
20      25      30
Lys Met Ser Tyr Gly Asn Lys Val Met Asp Phe Thr Pro Pro Thr Leu
35      40      45
Gln Asp Tyr Ile Val Gly Ile Gln Gly Gln Ser Ala Leu Asn Gln Ile
50      55      60
Glu Ala Val Gly Gly Asn Asn Ala Ile Lys Trp Leu Ser Thr Leu Met
65      70      75      80
Met Glu Thr Lys Glu Asn Pro Leu Phe Ala Pro Ile Tyr Leu Glu Asn
85      90      95
His Ser Leu Asn Glu Ile Leu Gly Val Thr Lys Asp Leu Gln Asn Thr
100      105      110
Ala Ser Leu Ile Ser Asn Pro Asn Phe Arg Asn Asn Ala Thr Ser Leu
115      120      125
Leu Glu Met Ala Ser Tyr Thr Gln Gln Thr Ser Arg Leu Thr Lys Leu
130      135      140
Ser Asp Phe Arg Ala Arg Glu Gly Glu Ser Asn Phe Ser Glu Arg Leu
145      150      155      160
Leu Glu Leu Lys Asn Lys Arg Phe Ser Asp Pro Asn Pro Ser Glu Val
165      170      175
Phe Val Lys Tyr Ser Gln Leu Ser Lys His Pro Asn Asn Leu Trp Ile
180      185      190
Gln Gly Val Gly Gly Ala Ser Phe Ile Ser Gly Gly Asn Gly Thr Leu
195      200      205
Tyr Gly Leu Asn Val Gly Tyr Asp Arg Leu Val Lys Ser Val Ile Leu
210      215      220
Gly Gly Tyr Val Ala Tyr Gly Tyr Ser Gly Phe Asn Gly Asn Ile Met
225      230      235      240
His Ser Leu Ala Asn Asn Val Asp Val Gly Met Tyr Ala Arg Ala Phe
245      250      255
Leu Lys Arg Asn Glu Phe Thr Leu Ser Ala Asn Glu Thr Tyr Gly Gly
260      265      270
Asn Ala Ser His Ile Asn Ser Ser Asn Ser Leu Leu Ser Val Leu Asn
275      280      285
Gln Arg Tyr Asn Tyr Asn Thr Trp Thr Thr Ser Val Asn Gly Asn Tyr
290      295      300
Gly Tyr Asp Phe Met Phe Lys Gln Lys Ser Val Val Leu Lys Pro Gln
305      310      315      320
Val Gly Leu Ser Tyr His Phe Ile Gly Leu Ser Gly Met Lys Gly Lys
325      330      335
Met Gln Asn Pro Ala Tyr Gln Gln Phe Val Met His Ser Asn Pro Ser
340      345      350
Asn Glu Ser Val Leu Thr Leu Asn Met Gly Leu Glu Ser Arg Lys Tyr
355      360      365
Phe Gly Lys Asn Ser Tyr Tyr Phe Val Thr Ala Arg Leu Gly Arg Asp
370      375      380
Leu Leu Ile Lys Ala Lys Gly Asp Asn Val Val Arg Phe Val Gly Glu
385      390      395      400
Asn Thr Leu Leu Tyr Arg Lys Gly Glu Ile Phe Asn Thr Phe Ala Ser
405      410      415

```

SUBSTITUTE SHEET (RULE 26)

1355

Val Ile Thr Gly Gly Glu Met His Leu Trp Arg Leu Met Tyr Val Asn
 420 425 430
 Ala Gly Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile
 435 440 445
 Thr Gly Asn Val Gly Met Arg Val Ala Phe
 450 455

(2) INFORMATION FOR SEQ ID NO:1829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...251

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1829

Thr Ile Leu Cys Pro Gly Ala Lys Ser Tyr Lys Tyr Trp Glu Gly Met
 1 5 10 15
 Gly Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr Thr
 20 25 30
 Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn Leu
 35 40 45
 Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr Leu
 50 55 60
 Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Lys Pro Val Gly Thr
 65 70 75 80
 Gly Pro Phe Lys Phe Phe Leu Trp Asn Lys Asp Glu Lys Ile Ile Leu
 85 90 95
 Val Lys Asn Gln Asp Tyr Trp Gly Leu Lys Ala Tyr Leu Asp Lys Val
 100 105 110
 Val Val Arg Thr Ile His Asn Phe Ser Thr Arg Ala Leu Ala Leu Arg
 115 120 125
 Thr Gly Glu Ile Met Leu Met Thr Gly His Asn Leu Asn Glu Val Glu
 130 135 140
 Gln Leu Glu Lys Leu His Asn Ile Val Val Asp Arg Ser Pro Gly Leu
 145 150 155 160
 Ile Ala Asn Trp Leu Ser Leu Asn Thr Gln Lys Lys Tyr Phe Asn Asn
 165 170 175
 Pro Leu Val Arg Leu Ala Ile Asn His Ala Ile Asn Val Asp Asp Tyr
 180 185 190
 Ile Lys Val Ile Tyr Glu Gly Phe Ala Gln Lys Met Val Asn Pro Phe
 195 200 205
 Pro Pro Thr Ile Trp Gly Tyr Asn Tyr Asn Ile Lys Pro Tyr Glu Tyr
 210 215 220
 Asp Leu Lys Lys Ala Lys Glu Leu Leu Lys Gln Ala Gly Tyr Pro Asn
 225 230 235 240
 Gly Phe Lys Thr Asn Ile Cys Thr Ser Leu Leu
 245 250

(2) INFORMATION FOR SEQ ID NO:1830:

(i) SEQUENCE CHARACTERISTICS:

SUBSTITUTE SHEET (RULE 26)

1356

(A) LENGTH: 879 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...879

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1830

```

Ile His Ile Lys Arg Ile Phe Leu Leu Lys Asn Thr Pro Phe Asn Pro
1      5      10      15
Pro Leu Phe Leu His Ile Ala Pro Leu Lys Pro Phe Met Ile Ile Ile
20      25      30
Asn Leu Phe Trp Asn Thr Phe Ser Leu Phe Val Lys Lys Thr Asn Lys
35      40      45
Asp Leu Ile Met Arg Val Thr Phe Gly Ser Lys Tyr Asn Gln Met Asn
50      55      60
His Tyr Gln Asn Ala Leu Gln Asn Lys Ile Asn Asp Ala Asn Thr Gln
65      70      75      80
Ile Ala Ser Gly Leu Lys Ile Arg Tyr Gly Tyr Gln Asn Ser Asp Ile
85      90      95
Asn Asn Gln Asn Leu Lys Phe Gln Tyr Glu Glu Asn Thr Leu Asp Gln
100     105     110
Gly Ile Asp Val Ala Gln Asn Ala Tyr Thr Ser Thr Leu Asn Thr Asp
115     120     125
Lys Ala Leu Gln Glu Phe Ser Lys Thr Met Glu Ala Phe Lys Thr Lys
130     135     140
Leu Ile Gln Ser Ala Asn Asp Val His Ser Glu Thr Ser Arg Ala Ala
145     150     155     160
Ile Ala Asn Asp Leu Glu Arg Leu Lys Glu His Met Ile Asn Val Ala
165     170     175
Asn Thr Ser Ile Gly Gly Glu Phe Leu Phe Gly Gly Ser Lys Val Asp
180     185     190
Arg Pro Pro Ile Asp Ser Asn Gly Lys Tyr His Gly Asn Gly Glu Asp
195     200     205
Leu Asn Ala Leu Ile Ser Ser Asp Asn Leu Val Pro Tyr Asn Ile Ser
210     215     220
Gly Gln Asp Leu Phe Leu Gly Thr Asp Lys Asp Lys His Lys Leu Ile
225     230     235     240
Thr Thr Asn Ile Lys Leu Leu Asn Gln Asn Lys Leu His Pro Asp Val
245     250     255
Met Asp Ala Leu Glu His Ser Ser Leu Pro Glu Glu Val Phe Ile Lys
260     265     270
Pro Ser Asp Thr Leu Arg Glu Leu Ile Gly Asp Asn Asp Lys Asn Pro
275     280     285
Thr Asn Asp Pro Lys Glu Phe Tyr Leu Gln Gly Ile Arg Pro Asp
290     295     300
Gly Ser Ser Phe Lys Glu Lys Phe Ala Leu Asp Lys Ala Tyr Gln Asn
305     310     315     320
Gln Glu Ser Ala Thr Lys Val Ser Asp Leu Leu Asp Lys Ile Gly His
325     330     335
Ala Tyr Gly Asn Thr Ser Gln Asn Lys Val Val Asp Val Ser Leu Asn
340     345     350
Asn Trp Gly Gln Ile Glu Ile Lys Asn Leu Thr Pro Gly Ser Glu Asn
355     360     365
Leu Asp Phe His Leu Ile Ser Ser Asp Gly Asp Phe Asp Asp Leu Asp
370     375     380

```

SUBSTITUTE SHEET (RULE 26)

1357

Ala Leu Arg Ser Ser Gly Lys Arg Val Thr Glu Tyr Val Lys Ser Ala
 385 390 395 400
 Phe Val Thr Asp Arg Ser Leu Ser Gln Val Lys Ala Val Pro Asn Met
 405 410 415
 Tyr Asn Pro Lys Val Leu Glu Ile Pro Ser Val Phe Val Thr Lys Asp
 420 425 430
 Asn Val Leu Ala Asn Lys Asn Thr Lys Leu Ser Glu Ile Phe Gly Asp
 435 440 445
 Lys Val Glu Thr Leu Lys Ile Asn Ala Ser Arg Leu Gly Asp Glu Ser
 450 455 460
 Ala Ile Lys Ile Pro Asn Leu Pro Ile Asn Leu Asp Ile Pro Ile Leu
 465 470 475 480
 Leu Asp Val Lys Asn Ser Thr Ile Lys Asp Leu Lys Asp Ala Ile Lys
 485 490 495
 Glu Arg Phe Asn Asn Glu Val Asp Val Glu Ile Glu Thr Asn Gly Arg
 500 505 510
 Leu Arg Ile Ile Asp Asn Ser Ser Lys Glu Ser Pro Ile Ser Phe Ala
 515 520 525
 Leu Ser Thr Leu Asp Gln Lys Gly Leu Glu Val Ala Gly Ile Pro Thr
 530 535 540
 Asn Asn Ala Ser Glu Tyr Gln Lys Thr Tyr Phe Asn Lys Glu Gly Ala
 545 550 555 560
 Lys Leu Glu Ser Asn Val Ala Gln Thr Ala Gln Asn Asp Ala Ala Asn
 565 570 575
 Gly Ser Thr Lys Leu Ser Glu Val Ser Lys Gly Ser Leu Glu Asn Ser
 580 585 590
 Val Phe Asn Met Lys Leu Asn Asp Val Asn Gly Ser Phe Leu Glu Ala
 595 600 605
 Gln Ile Asn Leu Asp Asn Asn Gly Ala Phe Leu Ser Leu Pro Asn Gly
 610 615 620
 Val Lys Ile Pro Leu Tyr Asp Pro Thr Thr Ala Asp Ile Gln Ala Ser
 625 630 635 640
 Lys Pro Asn Glu Val Thr Tyr Arg Gln Leu Met Asp Ala Met Ser Ile
 645 650 655
 Ala Leu Asn Tyr Ser Asn Thr Asp Pro Ala Ile Tyr Gln Gln Ile Ser
 660 665 670
 Asp Asn Pro Thr Ser Lys Glu Ser Lys Glu Arg Phe Ile Glu Leu Leu
 675 680 685
 Lys Gln Ala Lys Asp Asn Leu Ser Ile Asn Leu Asn Glu Glu Gly Lys
 690 695 700
 Val Ile Ile Gln Asp Asn Met His Ser Asn Thr Lys Met Gln Phe Met
 705 710 715 720
 Leu Phe Asp Lys Asp Ala Asn Asp Phe Ser Gln Asn Ala Leu His Ser
 725 730 735
 Asp Lys Pro Ser Leu Lys Leu Asn Ala Asn Asn Ala Leu Ile Ile Asp
 740 745 750
 Lys Pro Ser Val Asn Phe Phe Asp Gln Leu Glu Asn Ile Ile Thr Ser
 755 760 765
 Val Arg Lys Gly Ile Tyr Arg Pro Asp Ala Leu Gly Asp Thr Tyr Ser
 770 775 780
 Ser Asp Met Arg Asn Leu Gly Ile Gln Asn Gly Ile Thr Leu Ile Asp
 785 790 795 800
 His Leu Ser Asp His Ile Glu Lys Met Ile Ala Lys Asn Gly Ala His
 805 810 815
 Gly Lys Ala Phe Glu Asn Ile Ile Arg Arg Asn Glu Val Leu Lys Thr
 820 825 830
 Gln Val Gln Ser Ile Arg Gly Glu Thr Thr Gly Thr Asp Met Ala Glu
 835 840 845
 Thr Tyr Asn Lys Phe Ser Asn Leu Thr Asn Asn Tyr Asn Ala Val Leu
 850 855 860
 Ala Ser Thr Asn Lys Ile Asn Asn Leu Ser Leu Thr Lys Tyr Leu
 865 870 875

(2) INFORMATION FOR SEQ ID NO:1831:

SUBSTITUTE SHEET (RULE 26)

1358

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 181 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1831

```

Arg Ile Asp Gln Ile Lys Ile Met Lys Leu Val Ser Leu Ile Val Ala
1           5           10           15
Leu Val Phe Cys Cys Phe Leu Gly Ala Val Glu Leu Pro Gly Val Tyr
          20           25           30
Gln Thr Gln Glu Phe Leu Tyr Met Lys Ser Ser Phe Val Glu Phe Phe
          35           40           45
Glu His Asn Gly Lys Phe Tyr Ala Tyr Gly Ile Ser Asp Val Asp Gly
          50           55           60
Ser Lys Ala Lys Lys Asp Lys Leu Asn Pro Asn Pro Lys Leu Arg Asn
          65           70           75           80
Arg Ser Asp Lys Gly Val Val Phe Leu Ser Asp Leu Ile Lys Val Gly
          85           90           95
Glu Gln Ser Tyr Lys Gly Gly Lys Ala Tyr Asn Phe Tyr Asp Gly Lys
          100          105          110
Thr Tyr His Val Arg Val Thr Gln Asn Ser Asn Gly Asp Leu Glu Phe
          115          120          125
Thr Ser Ser Tyr Asp Lys Trp Gly Tyr Val Gly Asn Thr Phe Thr Leu
          130          135          140
Lys Arg Val Arg Gly Ala Glu Ile Ser Ile Leu Lys Leu Lys Arg Phe
          145          150          155          160
Asn Leu Met Arg Ser Phe Tyr Arg Gln Thr His Leu Phe Ser Ile Gly
          165          170          175
Lys Ala Tyr Ala Thr
          180

```

(2) INFORMATION FOR SEQ ID NO:1832:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 215 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1832

1359

```

Lys Asp Leu Ser Lys Met Phe Val Val Phe Ile Glu Gly Phe Gly Leu
1          5          10          15
Ala Ile Ser Leu Cys Ala Ala Val Gly Ala Gln Ser Leu Phe Ile Val
20          25          30
Glu Arg Gly Met Ala Arg Asn Tyr Val Phe Leu Ile Cys Ala Leu Cys
35          40          45
Phe Met Cys Asp Ile Val Leu Met Ser Met Gly Val Phe Gly Val Gly
50          55          60
Ala Tyr Phe Ala Lys Asn Leu Tyr Leu Ser Leu Phe Leu Asn Leu Phe
65          70          75          80
Gly Ala Val Phe Thr Gly Phe Tyr Ala Phe Leu Ala Leu Lys Thr Leu
85          90          95
Phe Gln Thr Phe Lys Lys Lys Gln Val Gln Thr Pro Lys Lys Leu Ser
100         105         110
Leu Lys Lys Thr Leu Leu Phe Thr Leu Gly Val Thr Leu Leu Asn Pro
115         120         125
Gln Val Tyr Leu Glu Met Val Phe Leu Ile Gly Ala Ser Ala Met Ser
130         135         140
Phe Asn Leu Val Gln Lys Phe Val Phe Leu Ala Gly Thr Leu Ser Ala
145         150         155         160
Ala Phe Ser Trp Leu Leu Leu Leu Cys Thr Met Ser Leu Arg Tyr Gly
165         170         175
Ser Lys Leu Leu Asn Asn Gln Lys Ile Phe Met Gly Val Asn Leu Phe
180         185         190
Val Thr Ala Ile Met Gly Thr Leu Ser Val Thr Leu Phe Arg Asp Phe
195         200         205
Leu Ala Leu Leu Ser Lys Thr
210         215

```

(2) INFORMATION FOR SEQ ID NO:1833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1833

```

Met Asp Ile Leu Lys Ala Glu His Leu Asn Lys Gln Ile Lys Lys Thr
1          5          10          15
Lys Ile Val Ser Asp Val Ser Leu Glu Val Lys Ser Gly Glu Val Val
20          25          30
Gly Leu Leu Gly Pro Asn Gly Ala Gly Lys Thr Thr Thr Phe Tyr Met
35          40          45
Ile Cys Gly Leu Leu Glu Pro Ser Gly Gly Ser Val Tyr Leu Asn Asp
50          55          60
Val Asp Leu Ala Lys Tyr Pro Leu His Lys Arg Ser Asn Leu Gly Ile
65          70          75          80
Gly Tyr Leu Pro Gln Glu Ser Ser Ile Phe Lys Glu Leu Ser Val Glu
85          90          95
Glu Asn Leu Ala Leu Ala Gly Glu Ser Thr Phe Lys Asn Ser Lys Glu
100         105         110
Ser Glu Glu Lys Met Glu Ser Leu Leu Asp Ala Phe Asn Ile Gln Ala

```

SUBSTITUTE SHEET (RULE 26)

		115					120					125				
Ile	Arg	Glu	Arg	Lys	Gly	Met	Ser	Leu	Ser	Gly	Gly	Glu	Arg	Arg	Arg	
	130					135					140					
Val	Glu	Ile	Ala	Arg	Ala	Leu	Met	Lys	Asn	Pro	Lys	Phe	Val	Leu	Leu	
145					150						155					160
Asp	Glu	Pro	Phe	Ala	Gly	Val	Asp	Pro	Ile	Ala	Val	Ile	Asp	Ile	Gln	
				165						170					175	
Arg	Ile	Ile	Glu	Ser	Leu	Ile	Gly	Leu	Asn	Ile	Gly	Val	Leu	Ile	Thr	
			180					185					190			
Asp	His	Asn	Val	Arg	Glu	Thr	Leu	Ser	Val	Cys	His	Arg	Ala	Tyr	Val	
		195					200					205				
Ile	Lys	Ser	Gly	Thr	Leu	Leu	Ala	Ser	Gly	Asn	Ala	Asn	Glu	Ile	Tyr	
	210					215					220					
Glu	Asn	Ala	Leu	Val	Arg	Lys	Tyr	Tyr	Leu	Gly	Glu	Asn	Phe	Lys	Val	
225					230					235						240

Asn	Thr	Gly	Leu	Trp	His	Ser	Trp	Gly	Leu	Ala	Pro	Ala	Leu	Leu	Glu
1				5					10					15	
Thr	Gln	Leu	Pro	Lys	His	Ala	His	Gln	Phe	Phe	Gln	Ile	Phe	Phe	Phe
		20						25					30		
Pro	Lys	Lys	Pro	Phe	Lys	Gln	Met	Ile	Val	Ile	Val	Glu	Leu	Leu	Val
		35					40					45			
Asn	Phe	Ile	Phe	Asn	Leu	Phe	His	Ala	Ile	His	Val	Gly	Val	Lys	Met
	50					55				60					
Ile	Asp	Asn	Ile	Lys	Leu	Pro	Leu	Arg	Arg	Ile	Lys	Met	Arg	Ala	Leu
65					70					75					80

(A) NAME/KEY: misc_feature

1361

(B) LOCATION 1...548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1835

```

Ile Asp Leu Gly Val Ile Glu Thr Ile Pro Lys His Ser Lys Ile Val
1      5      10      15
Leu Pro Gly Glu Ala Phe Asp Ser Leu Lys Glu Ala Phe Asp Lys Ile
      20      25      30
Asp Pro Tyr Thr Phe Phe Phe Pro Lys Phe Glu Ala Thr Ser Thr Ser
      35      40      45
Ile Ser Asp Thr Asn Thr Gln Arg Val Phe Glu Thr Leu Asn Asn Ile
      50      55      60
Lys Thr Asn Leu Ile Met Lys Tyr Ser Asn Glu Asn Pro Asn Asn Phe
      65      70      75      80
Asn Thr Cys Pro Tyr Asn Asn Asn Gly Asn Thr Lys Asn Asp Cys Trp
      85      90      95
Gln Asn Phe Thr Pro Gln Thr Ala Glu Glu Phe Thr Asn Leu Met Leu
      100      105      110
Asn Met Ile Ala Val Leu Asp Ser Gln Ser Trp Gly Asp Ala Ile Leu
      115      120      125
Asn Ala Pro Phe Glu Phe Thr Asn Ser Ser Thr Asp Cys Asp Ser Asp
      130      135      140
Pro Ser Lys Cys Val Asn Pro Gly Val Asn Gly Arg Val Asp Thr Lys
      145      150      155      160
Val Asp Gln Gln Tyr Ile Leu Asn Lys Gln Gly Ile Ile Asn Asn Phe
      165      170      175
Arg Lys Lys Ile Glu Ile Asp Ala Val Val Leu Lys Asn Ser Gly Val
      180      185      190
Val Gly Leu Ala Asn Gly Tyr Gly Asn Asp Gly Glu Tyr Gly Thr Leu
      195      200      205
Gly Val Glu Ala Tyr Ala Leu Asp Pro Lys Lys Leu Phe Gly Asn Asp
      210      215      220
Leu Lys Thr Ile Asn Leu Glu Asp Leu Arg Thr Ile Leu His Glu Phe
      225      230      235      240
Ser His Thr Lys Gly Tyr Gly His Asn Gly Asn Met Thr Tyr Gln Arg
      245      250      255
Val Pro Val Thr Lys Asp Gly Gln Val Glu Lys Asp Ser Asn Gly Lys
      260      265      270
Pro Lys Asp Ser Asp Gly Leu Pro Tyr Asn Val Cys Ser Leu Tyr Gly
      275      280      285
Gly Phe Asn Gln Pro Ala Phe Pro Ser Asn Tyr Pro Asn Ser Ile Tyr
      290      295      300
His Asn Cys Ala Asp Val Pro Ala Gly Phe Leu Gly Val Thr Ala Ala
      305      310      315      320
Val Trp Gln Gln Leu Ile Asn Gln Asn Ala Leu Pro Ile Asn Tyr Ala
      325      330      335
Asn Leu Gly Ser Gln Thr Asn Tyr Asn Leu Asn Ala Ser Leu Asn Thr
      340      345      350
Gln Asp Leu Ala Asn Ser Met Leu Ser Thr Ile Gln Lys Thr Phe Val
      355      360      365
Thr Ser Ser Val Thr Asn His His Phe Ser Asn Ala Ser Gln Ser Phe
      370      375      380
Arg Ser Pro Ile Leu Gly Val Asn Ala Lys Ile Gly Tyr Gln Asn Tyr
      385      390      395      400
Phe Asn Asp Phe Ile Gly Leu Ala Tyr Tyr Gly Ile Ile Lys Tyr Asn
      405      410      415
Tyr Ala Lys Ala Val Asn Gln Lys Val Gln Gln Leu Ser Tyr Gly Gly
      420      425      430
Gly Ile Asp Leu Leu Leu Asp Phe Ile Thr Thr Tyr Ser Asn Lys Asn
      435      440      445
Ser Pro Thr Gly Ile Gln Thr Lys Arg Asn Phe Ser Ser Ser Phe Gly
      450      455      460
Ile Phe Gly Gly Leu Arg Gly Leu Tyr Asn Ser Tyr Tyr Val Leu Asn
      465      470      475      480
Lys Val Lys Gly Ser Gly Asn Leu Asp Val Ala Thr Gly Leu Asn Tyr

```

SUBSTITUTE SHEET (RULE 26)

1362

```

          485          490          495
Arg Tyr Lys His Ser Lys Tyr Ser Val Gly Ile Ser Ile Pro Leu Ile
          500          505          510
Gln Arg Lys Ala Ser Val Val Ser Ser Gly Gly Asp Tyr Thr Asn Ser
          515          520          525
Phe Val Phe Asn Glu Gly Ala Ser His Phe Lys Val Phe Phe Asn Tyr
          530          535          540
Gly Trp Val Phe
545

```

(2) INFORMATION FOR SEQ ID NO:1836:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1836

```

Asp His Ser Phe Asn Ile Gln Asn Ser Ile Lys Arg Lys Val Met Tyr
1          5          10          15
Ala Ala His Pro Ile Lys Pro Ile Lys Ala Pro Lys Leu Lys Ser Gln
20          25          30
Phe Leu Arg Arg Val Phe Val Gly Ala Ser Ile Arg Arg Trp Asn Asp
35          40          45
Gln Ala Cys Pro Leu Glu Phe Val Glu Leu Asp Lys Gln Ala His Lys
50          55          60
Ala Met Ile Ala Tyr Leu Leu Ala Lys Asp Leu Lys Asp Arg Gly Lys
65          70          75          80
Asp Leu Asp Leu Asp Leu Leu Ile Lys Tyr Phe Cys Phe Glu Phe Leu
85          90          95
Glu Arg Leu Val Leu Thr Asp Ile Lys Pro Pro Ile Phe Tyr Ala Leu
100          105          110
Gln Gln Thr His Ser Lys Glu Leu Ala Ser Tyr Val Ala Gln Ser Leu
115          120          125
Gln Asp Glu Ile Ser Ala Tyr Phe Ser Leu Glu Glu Leu Lys Glu Tyr
130          135          140
Leu Ser His Arg Pro Gln Ile Leu Glu Thr Gln Ile Leu Glu Ser Ala
145          150          155          160
His Phe Tyr Ala Ser Lys Trp Glu Phe Asp Ile Ile Tyr His Phe Asn
165          170          175
Pro Asn Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln
180          185          190
Leu His Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu
195          200          205
Asp Leu Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys
210          215          220
Arg Trp Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His
225          230          235          240
Thr Leu Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys
245          250          255
Ala Cys Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe His
260          265          270

```

SUBSTITUTE SHEET (RULE 26)

1363

```

Asp Leu Pro Glu Ile Leu Thr Arg Asp Ile Ile Thr Pro Ile Lys Gln
  275                280                285
Ser Val Ala Gly Leu Asp His Cys Ile Lys Glu Ile Glu Lys Lys Glu
  290                295                300
Met Gln Asn Lys Val Tyr Ser Phe Val Ser Leu Gly Val Gln Glu Asp
  305                310                315                320
Leu Lys Tyr Phe Thr Glu Asn Glu Phe Lys Asn Arg Tyr Lys Asp Lys
                325                330                335
Ser His Gln Ile Val Phe Thr Lys Asp Ala Glu Glu Leu Phe Thr Leu
                340                345                350
Tyr Asn Ser Asp Glu Tyr Leu Gly Val Cys Gly Glu Leu Leu Lys Val
                355                360                365
Cys Asp His Leu Ser Ala Phe Leu Glu Ala Gln Ile Ser Leu Ser His
  370                375                380
Gly Ile Ser Ser Tyr Asp Leu Ile Gln Gly Ala Lys Asn Leu Leu Glu
  385                390                395                400
Leu Arg Ser Gln Thr Glu Leu Leu Asp Leu Asp Leu Gly Lys Leu Phe
                405                410                415
Arg Asp Phe Lys
                420

```

(2) INFORMATION FOR SEQ ID NO:1837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...268

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1837

```

Asn Ile Thr Ile Lys Asp Arg Thr Met Lys Thr Asn Gly His Phe Lys
  1                5                10                15
Asp Phe Ala Trp Lys Lys Cys Phe Leu Gly Ala Ser Val Val Ala Leu
  20                25                30
Leu Val Gly Cys Ser Pro His Ile Glu Thr Asn Glu Val Ala Leu
  35                40                45
Lys Leu Asn Tyr His Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu
  50                55                60
Lys Ile Leu Leu Leu Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala
  65                70                75                80
Lys Glu Tyr Glu Asn Lys Phe Lys Asn Gln Thr Thr Leu Lys Val Glu
  85                90                95
Glu Ile Leu Gln Asn Gln Gly Tyr Lys Val Ile Asn Val Asp Ser Ser
  100               105               110
Asp Lys Asp Asp Phe Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala
  115               120               125
Val Ala Met Asn Gly Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr
  130               135               140
Ile Gln Lys Lys Ser Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp
  145               150               155               160
Lys Met Glu Arg Val Leu Ile Pro Ala Gly Phe Val Lys Val Thr Ile
  165               170               175
Leu Lys Pro Met Ser Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu

```

SUBSTITUTE SHEET (RULE 26)

1364

```

          180          185          190
Ser Glu Leu Asp Ile Gln Glu Lys Phe Leu Lys Thr Thr His Ser Ser
          195          200          205
His Ser Gly Gly Leu Val Ser Thr Met Val Lys Gly Thr Asp Asn Ser
          210          215          220
Asn Asp Ala Ile Lys Ser Ala Leu Asn Lys Ile Phe Ala Ser Ile Met
          225          230          235          240
Gln Glu Met Asp Lys Lys Leu Thr Gln Arg Asn Leu Glu Ser Tyr Gln
          245          250          255
Lys Asp Ala Lys Glu Leu Lys Asn Lys Arg Asn Arg
          260          265

```

(2) INFORMATION FOR SEQ ID NO:1838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1838

```

Ser Asn Phe Lys Lys Gly Phe Phe Met Phe Lys Ser Arg Leu Asn Ser
1          5          10          15
Trp Ile Leu Leu Gly Ile Leu Gly Val Leu Val Val Phe Trp Asp
          20          25          30
Val Ile Lys Tyr Lys Ile Glu Asp Leu Gln His Asp His Tyr Leu Ser
          35          40          45
Gln Val Lys Glu Arg Glu Glu Tyr Tyr Lys Asn His Ile Glu Glu Ala
          50          55          60
Leu Lys Lys Asp Ser Glu Cys Phe Glu Lys Gly Gly Asp Lys Val Asp
          65          70          75          80
Cys Ser Ala Ala Met Arg Ile Ala Ala Gly Glu Arg Asn Arg Arg Met
          85          90          95
Leu Glu Ile Lys
          100

```

(2) INFORMATION FOR SEQ ID NO:1839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

1365

(B) LOCATION 1...242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1839

```

Lys Leu Phe Leu Val Ile Ile Phe Gln Lys Thr Leu Arg Glu Ile Met
1      5      10      15
Gln Asp Leu Gln His Phe Lys Asn Asp Ile Thr Leu Ile Leu Ser Lys
20      25      30
Asp Arg Leu Asp Thr Tyr Asp Ser Leu Glu Gln Tyr Lys Glu Asn Leu
35      40      45
Lys Leu Ile Ala Phe Ile Thr Pro Lys Ile Ser Asn Leu Glu Ile Tyr
50      55      60
Leu Arg Asn Ala Leu Asp Tyr Cys Leu Thr Gln Met Lys Gly Ser Glu
65      70      75      80
Trp Val Phe Asn Glu Ser Val Leu Thr Pro Leu Ile Lys Glu Leu Lys
85      90      95
Glu Lys Lys Lys Glu Ile Thr His Ser Leu Ile Leu Ser Lys Met Ser
100     105     110
Leu Gly Ala Val Ile Arg Leu Ile Phe Cys Tyr Lys Leu Glu Gly Val
115     120     125
Ile Leu Asp Leu Lys Arg Ile Asn Phe Lys Ser Tyr Tyr Pro Asn Asn
130     135     140
Lys Asn Ala Leu Phe Ile Asn Asn Lys Lys Asn Pro Leu Ser Ser Ala
145     150     155     160
Ser Lys Val His Ile Ala Leu Asn Leu Leu Trp Thr Ile Arg Asn Arg
165     170     175
Ala Tyr His Trp Glu Asn Leu Leu Lys Ile Gln Pro Asn Lys Arg Pro
180     185     190
Arg Ile Thr Thr Tyr Phe Ile Gly Leu Lys Asp Asn Asp Arg Ala Arg
195     200     205
Ile Pro Met Asn Ile Ser Val Glu Pro Ser Lys Ile Val Leu Phe Leu
210     215     220
Asp Asp Leu Ile Lys Ser Ile Gly Asn Lys Asp Leu Glu Asp Leu Ser
225     230     235     240
Ser Leu

```

(2) INFORMATION FOR SEQ ID NO:1840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1840

```

Gly Met Lys Ala Leu Lys Thr Phe Leu Lys Lys Ser Leu Ile Leu Leu
1      5      10      15
Leu Ala Ile Ala Leu Asn His Leu Asn Ala Val Ala Met Ile Val Asp
20      25      30
Asn Pro Thr Gln Asn Ala Trp Asn Gly Ala Lys Arg Ala Trp Asp Glu
35      40      45
Ser Lys Trp Ala Lys His Leu Ala Thr Ile Thr Glu Arg Ile Lys Leu

```

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50	55	60
Ala Gln Asp Thr Leu	Asp Arg Ala Asn Gln Thr	Leu Asn Ser Ile Asn
65	70	75
Lys Val Asn Asp Val	Leu Asn Lys Thr	Asn Gln Phe Leu Thr
85	90	95
Ile Leu Ser Ile Pro	Asn Pro Met Gln Tyr	Val Glu Lys Ile Gln Ser
100	105	110
Phe Ala Lys Gln Val	Gln Ala Asn Thr	Glu Arg Ile Lys Glu Asn Ala
115	120	125
Gln Asn Tyr Asp Ile	Arg Asn Gln Ile	Ala Ala Lys Arg Ile Ser Glu
130	135	140
Lys Cys Pro Glu Leu	Asn Trp Asp Val	Ser Gln Asp Ala Ser Pro Thr
145	150	155
Glu Lys Asn Leu His	Gln Phe Phe Thr	Ser Lys Gly Lys Glu Ser Ala
165	170	175
Asn Thr Lys Ala Leu	Lys Asp Phe Ala	Asn Ala Ile Gly Asn Thr Gln
180	185	190
Ile Ser Thr Ala Asn	Asp Leu Gly Ala	Gly Leu Arg Gly Arg Ala Leu
195	200	205
Leu Glu Tyr Ile Cys	Ile Gln Lys Gly	Asn Leu Glu Ala Ala Lys Lys
210	215	220
Ile Gln Leu Leu Asp	Ser Gln Met Thr	Leu Ala Leu Leu Asn Asn Asp
225	230	235
Tyr Thr Ala Tyr Glu	Lys Leu Arg Ala	Glu Lys Glu Glu Leu Lys Arg
245	250	255
Gln Ile Ala Ser Asn	Val Tyr Ala Lys	Val Lys Gln Leu Val Val Ala
260	265	270
Ser Gln Asp Arg Ala	Phe Ser Gln Met	Asp Asn Glu Leu Gly Val Lys
275	280	285
Thr Phe Gly Phe Asn	Asp Glu Asn Val	Lys Lys Gly Tyr Cys Lys Lys
290	295	300
Glu Asn Arg Asn Gly	Lys Ser Glu Cys Ile	Pro Asn Met Leu Asn Val
305	310	315
Asn Arg Leu Lys Ala	Gln Phe Asp Glu	Leu Asn Leu Asp Tyr Ser Arg
325	330	335
Asp Ile Ala Gly Lys	Lys Gly Glu Ala	Ala Ala Lys Val Phe Asn Asp
340	345	350
Tyr Lys His Arg Phe	Gln Gln Leu Ser	Val Glu Thr Ala Leu Glu Ile
355	360	365
Ala Gln Asn Leu Ser	Phe Met Asn Lys	Thr Leu Gly Leu Met Val Gln
370	375	380
Met Gln Ser Tyr Ala	Phe Lys Gln Gln	Met Gly Tyr Phe Glu Asp Ile
385	390	395
Ile Pro Ala Asp Ala	Leu Lys Asp Asp	Lys Glu His Gln Glu Asn Leu
405	410	415
Glu Gln Lys Gln Gln	Glu Ile Glu Lys	Val Tyr Arg Ala Lys Leu Asp
420	425	430
Ala Tyr Gly Phe Pro	Asn Gly Ser Val	Gly Lys Ala Ser Gly Val Asn
435	440	445
Ser Asn Ser Asn Asn	Glu Ala Pro Ser	Ser Asp Asn Ile Gln Ser Phe
450	455	460
Asn Pro Tyr		
465		

(2) INFORMATION FOR SEQ ID NO:1841:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1841

```

Arg Leu Asn Asn Met Ala Ala Pro Leu Leu Ala Leu Pro Phe Leu Ser
1      5      10      15
Asn Pro Leu Val Leu Gly Ala Leu Ala Val Ile Gly Val Gly Ala Tyr
20      25      30
Leu Tyr Pro Asn Lys Gln Asp Ser Leu Val Val Gln Ala Asp Gly Leu
35      40      45
Tyr Ser Glu Ile Leu Gly Phe Phe Ile Ser Phe Ser Ser Lys Ile Leu
50      55      60
Lys Gly Ile Gly Glu Pro Leu Ala Asn Val Ile Gln Pro Phe Gly Met
65      70      75      80
Val Leu Gly Met Leu Leu Ile Leu Leu Tyr Ser Phe Lys Arg Tyr Gln
85      90      95
Asn Asn Asp Leu Phe Glu Ile Lys Thr Phe Leu Met Leu Phe Val Phe
100     105     110
Val Gly Tyr Leu Ser Leu Tyr His Tyr Ala Phe Lys Ser Asp Gly Ser
115     120     125
Ser Ser Gly Asn Gly Arg Ser Ser Phe Ala Phe Gln Asn His Val Thr
130     135     140
Glu Ile Phe Asp Thr Pro Ala Asn Leu Leu Asn Ala Gly Ile Ser Asn
145     150     155     160
Val Val Lys Glu Tyr Gln Thr Asn Ser Ala Arg Glu His Lys Asn Ile
165     170     175
Asp Thr His His Ser Ile Thr Asn Ala Asn Ile Ser Phe His Val Arg
180     185     190
Gln Ile Leu Thr Ser Leu Asn Lys Leu Tyr Glu Asp Phe Lys Ile Asn
195     200     205
Asn Gly Leu Ser Leu Lys Thr Leu Ile Ala Ala Val Leu Leu Leu Val
210     215     220
Ile Leu Gly Leu Glu Leu Phe Leu Leu Phe Lys Val Phe Cys Tyr Val
225     230     235     240
Phe Met Thr Tyr Leu Glu Lys Ile Ile Tyr Leu Ser Leu Val Ile Phe
245     250     255
Met Leu Leu Leu Gly Phe Phe Gln Gln Thr Arg Gly Phe Leu Val Ser
260     265     270
Tyr Val Lys Lys Ile Ile Ser Leu Thr Phe Tyr Met Pro Leu Leu Leu
275     280     285
Leu Leu Val Leu Phe Asn Ser Phe Ala Leu Gln Tyr Ala Ile Lys Val
290     295     300
Gly Gly Ser Asn Glu Ile Val Ala Lys Phe Gly Ile Ile Val Ala Ile
305     310     315     320
Gly Ile Ser Leu Thr Phe Ile Gln Lys Val Pro Glu Met Ile Asn Ala
325     330     335
Ile Phe Gly Thr Gln Gly Gly Leu Thr Asp Ala Lys Ser Phe Ile Tyr
340     345     350
Gln Gly Val Gln Met Ala Ser Ala Gly Ala Gly Ala Ile Ala Gly Ser
355     360     365
Leu Lys Ser Val Gly Arg Ser Ala Phe Gly Arg Thr Leu Glu Ala Tyr
370     375     380
Lys Asp Ala Lys Ser Thr Ile Asn Ser Thr Thr Ala Asn Met Arg Asp
385     390     395     400
Met Pro Gly His Pro Gly Val Arg Val Gly Val Glu Thr Ile Glu Leu
405     410     415
Pro Lys Ser His Arg Ala Ser Lys
420

```

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(2) INFORMATION FOR SEQ ID NO:1842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1842

```

Lys Asn Arg Tyr Leu Lys Arg Gly Arg Asn Ala Ile Leu Glu Pro Ser
1      5      10      15
Arg Asn Arg Leu Lys His Ala Ala Phe Phe Val Gly Leu Phe Ile Val
20      25      30
Leu Phe Leu Ile Ile Met Lys His Gln Thr Ser Pro Tyr Ala Phe Thr
35      40      45
His Asn Gln Ala Leu Val Thr Gln Thr Pro Pro Tyr Phe Thr Gln Leu
50      55      60
Thr Ile Pro Lys Pro Asn Asp Ala Leu Ser Ala His Ala Ser Ser Leu
65      70      75      80
Ile Ser Leu Pro Asn Asp Asn Leu Leu Ser Ala Tyr Phe Ser Gly Thr
85      90      95
Lys Glu Gly Ala Arg Asp Val Lys Ile Ser Ala Asn Leu Phe Asp Ser
100     105     110
Lys Thr Asn Arg Trp Ser Glu Ala Phe Ile Leu Leu Thr Lys Glu Glu
115     120     125
Leu Ser His His Ser His Glu Tyr Ile Lys Lys Leu Gly Asn Pro Leu
130     135     140
Leu Phe Leu His Asp Asn Lys Ile Leu Leu Phe Val Val Gly Val Ser
145     150     155     160
Met Gly Gly Trp Ala Thr Ser Lys Ile Tyr Gln Phe Glu Ser Ala Leu
165     170     175
Glu Pro Ile His Phe Lys Phe Ala Arg Lys Leu Ser Leu Ser Pro Phe
180     185     190
Leu Asn Leu Ser His Leu Val Arg Asn Lys Pro Leu Asn Thr Thr Asp
195     200     205
Gly Gly Phe Met Leu Pro Leu Tyr His Glu Leu Ala Thr Gln Tyr Pro
210     215     220
Leu Leu Leu Lys Phe Asp Gln Gln Asn Asn Pro Arg Glu Leu Leu Arg
225     230     235     240
Pro Asn Thr Leu Asn His Gln Leu Gln Pro Ser Leu Thr Pro Phe Lys
245     250     255
Asp Cys Ala Val Met Ala Phe Arg Asn His Ser Phe Lys Asp Ser Leu
260     265     270
Met Leu Glu Thr Cys Lys Thr Pro Thr Asp Trp Gln Lys Pro Ile Ser
275     280     285
Thr Asn Leu Lys Asn Leu Asp Ser Leu Asn Leu Leu Asn Leu Asn
290     295     300
Gly Ile Leu Tyr Leu Ile His Asn Pro Ser Asp Leu Ser Leu Arg Arg
305     310     315     320
Lys Glu Leu Trp Leu Ser Lys Leu Glu Asn Ser Asn Ser Phe Lys Thr
325     330     335
Leu Lys Val Leu Asp Lys Ala Asn Glu Val Ser Tyr Pro Ser Tyr Ser
340     345     350

```

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Leu Asn Pro His Phe Ile Asp Ile Val Tyr Thr Tyr Asn Arg Ser His
 355 360 365
 Ile Lys His Ile Arg Phe Asn Met Ala Tyr Leu Asn Ser Leu Leu Lys
 370 375 380

(2) INFORMATION FOR SEQ ID NO:1843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1843

Leu Val Met Phe Ile Ser Ser Ser Tyr Thr Leu Ser Phe Val Trp Leu
 1 5 10 15
 Phe Leu Ile Phe Phe Phe Lys Asn Lys Pro Leu Gly Leu Arg Phe
 20 25 30
 Ser Leu Ser Leu Ile Ser Val Ile Leu Ser Asn Ile Ala Leu Lys Asp
 35 40 45
 Ser Leu Ser Leu Asn Glu Phe Leu Ser Ser Phe Thr Ala Pro Leu Ser
 50 55 60
 Pro Phe Ser Cys Leu Leu Ile Leu Ala Tyr Ala Ser Phe Ser Cys His
 65 70 75 80
 Ile Leu Lys Lys Pro Pro Leu Glu Thr Leu Gln Ser Tyr Ser Val Met
 85 90 95
 Leu Phe Phe Asn Leu Leu Leu Thr Asp Ile Leu Gly Phe Leu Pro
 100 105 110
 Phe Ser Ile Tyr His His Phe Met Ala Ser Leu Ile Phe Ser Ala Leu
 115 120 125
 Phe Cys Ser Ser Leu Phe Leu Ser Ser Pro Leu Leu Gly Val Ile Ala
 130 135 140
 Leu Val Ala Leu Ser Ser Ser Leu Leu Met Arg Ser Asn Phe Gln Ile
 145 150 155 160
 Leu Asp Ser Leu Leu Asp Phe Pro Leu Phe Leu Phe Val Phe Phe Lys
 165 170 175
 Thr Leu Tyr Leu Ala Lys Lys Arg Leu
 180 185

(2) INFORMATION FOR SEQ ID NO:1844:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 982 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1844

```

Lys Arg Ile Leu Met Lys Lys Arg Lys His Val Ser Lys Lys Val Phe
1      5      10      15
Asn Val Ile Ile Leu Phe Val Ala Val Phe Thr Leu Leu Val Val Ile
      20      25      30
His Lys Thr Leu Ser Asn Gly Ile His Ile Gln Asn Leu Lys Ile Gly
      35      40      45
Lys Leu Gly Ile Ser Glu Leu Tyr Leu Lys Leu Asn Asn Lys Leu Ser
      50      55      60
Leu Glu Val Glu Arg Val Asp Leu Ser Ser Phe Phe His Gln Lys Pro
      65      70      75      80
Thr Lys Lys Arg Leu Glu Val Ser Asp Leu Ile Lys Asn Ile Arg Tyr
      85      90      95
Gly Ile Trp Ala Val Ser Tyr Phe Glu Lys Leu Lys Val Lys Glu Ile
      100      105      110
Ile Leu Asp Asp Lys Asn Lys Ala Asn Ile Phe Phe Asp Gly Asn Lys
      115      120      125
Tyr Glu Leu Glu Phe Pro Gly Ile Lys Gly Glu Phe Ser Leu Glu Asp
      130      135      140
Asp Lys Asn Ile Lys Leu Lys Ile Ile Asn Leu Leu Phe Lys Asp Val
      145      150      155      160
Lys Val Gln Val Asp Gly Asn Ala His Tyr Ser Pro Lys Ala Arg Lys
      165      170      175
Met Ala Phe Asn Leu Ile Val Lys Pro Leu Val Glu Pro Ser Ala Ala
      180      185      190
Ile Tyr Leu Gln Gly Leu Thr Asp Leu Lys Thr Ile Glu Leu Lys Ile
      195      200      205
Asn Thr Ser Pro Met Lys Ser Leu Ala Phe Leu Lys Pro Leu Phe Gln
      210      215      220
Arg Gln Ser Gln Lys Asn Leu Lys Thr Trp Ile Phe Asp Lys Ile Gln
      225      230      235      240
Phe Ala Ser Phe Lys Ile Asp Asn Ala Leu Ile Lys Ala Asn Phe Thr
      245      250      255
Pro Ser Glu Phe Ile Pro Ser Leu Leu Glu Asn Ser Val Val Lys Ala
      260      265      270
Thr Leu Ile Lys Pro Ser Val Val Phe Asn Asp Gly Leu Ser Pro Ile
      275      280      285
Lys Met Asp Lys Thr Glu Leu Ile Phe Lys Asn Lys Gln Leu Leu Ile
      290      295      300
Gln Pro Gln Lys Ile Thr Tyr Glu Thr Met Glu Leu Thr Gly Ser Tyr
      305      310      315      320
Ala Thr Phe Ser Asn Leu Leu Glu Ala Pro Lys Leu Glu Val Phe Leu
      325      330      335
Lys Thr Thr Pro Asn Tyr Tyr Gly Asp Ser Ile Lys Asp Leu Leu Ser
      340      345      350
Ala Tyr Lys Val Val Leu Pro Leu Asp Lys Ile Ser Met Pro Ser Ser
      355      360      365
Ala Asp Leu Lys Leu Thr Leu Gln Phe Leu Lys Asn Thr Ala Pro Leu
      370      375      380
Phe Ser Val Gln Gly Ser Val Asn Leu Gln Glu Gly Thr Phe Ser Leu
      385      390      395      400
Tyr Asn Ile Pro Leu Tyr Thr Gln Ser Ala Gln Ile Asn Leu Asp Ile
      405      410      415
Ala Gln Glu Tyr Gln Tyr Ile Tyr Ile Asp Thr Ile His Thr Arg Tyr
      420      425      430
Ala Asn Met Leu Asp Leu Asp Ala Lys Ile Ala Leu Asp Leu Gly Gln
      435      440      445
Lys Asn Leu Ser Leu Asp Ser Leu Val His Lys Ile Gln Val Asn Thr
      450      455      460

```


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Asn	Asn	Asn	Ile	Asn	Met	Arg	Ser	Tyr	Asp	Pro	Asn	Asn	Thr	Gln	Glu
465					470					475					480
Asp	Pro	Gln	Thr	Asn	Phe	Thr	Leu	Asp	Leu	Lys	Ser	Leu	His	Ser	Ile
				485					490						495
Ile	Gln	Glu	Gly	Glu	Asn	Ser	Glu	Val	Phe	Arg	Arg	Lys	Ile	Ile	Asp
			500					505					510		
Thr	Ile	Lys	Ala	Gln	Ser	Glu	Asp	Lys	Phe	Thr	Lys	Asp	Val	Phe	Tyr
		515					520					525			
Ala	Thr	Gly	Asp	Thr	Leu	Lys	Ser	Leu	Ser	Leu	Ser	Phe	Asp	Phe	Ser
	530					535					540				
Asn	Pro	Asp	His	Ile	Gln	Trp	Ser	Val	Pro	Gln	Leu	Leu	Leu	Glu	Gly
545					550					555					560
Glu	Phe	Lys	Asp	Asn	Ala	Tyr	Thr	Phe	Lys	Ile	Lys	Asp	Leu	Lys	Lys
				565					570						575
Ile	Lys	Pro	Tyr	Ser	Pro	Ile	Met	Asp	Tyr	Ile	Ala	Leu	Lys	Asp	Gly
			580					585					590		
Ser	Leu	Glu	Val	Ser	Thr	Ser	Asp	Phe	Val	Asn	Ile	Asp	Phe	Phe	Ala
		595					600					605			
Lys	Asp	Leu	Lys	Ile	Asn	Leu	Pro	Ile	Tyr	Arg	Ser	Asp	Gly	Ser	His
	610					615					620				
Phe	Asp	Ser	Phe	Ser	Leu	Phe	Gly	Ser	Ile	Asn	Lys	Asp	Glu	Ile	Ser
625					630					635					640
Val	Tyr	Thr	Pro	Ser	Lys	Ser	Ile	Ser	Ile	Lys	Val	Lys	Gly	Asp	Gln
				645					650						655
Lys	Asp	Ile	Thr	Leu	Asn	Asn	Ile	Asp	Leu	Ser	Ile	Asp	Asp	Phe	Leu
			660					665					670		
Asp	Ser	Lys	Met	Pro	Ala	Ile	Ala	Gly	Leu	Phe	Ser	Lys	Glu	Arg	Lys
		675					680					685			
Glu	Lys	Pro	Ser	Ser	Lys	Glu	Ile	Gln	Asp	Glu	Asp	Val	Phe	Ile	Ser
	690					695					700				
Ala	Lys	Gln	Arg	Tyr	Glu	Lys	Ala	His	Lys	Ile	Ile	Pro	Ile	Ser	Thr
705					710					715					720
Arg	Ile	His	Ala	Lys	Asp	Val	Val	Leu	Ile	Tyr	Lys	Lys	Met	Pro	Phe
				725					730					735	
Pro	Leu	Glu	Asn	Leu	Asp	Ile	Val	Ala	Gln	Asp	Asp	Arg	Val	Lys	Ile
			740					745					750		
Asp	Gly	Asn	Tyr	Lys	Asn	Ala	Met	Ile	Met	Ala	Asp	Leu	Val	His	Gly
		755					760					765			
Ala	Leu	Tyr	Leu	Lys	Ala	His	Asn	Phe	Ser	Gly	Asp	Tyr	Ile	Asn	Thr
	770					775					780				
Ile	Leu	Gln	Lys	Asp	Phe	Val	Glu	Gly	Gly	Leu	Phe	Thr	Leu	Ile	Gly
785					790					795					800
Ala	Leu	Glu	Asp	Gln	Val	Phe	Asn	Gly	Glu	Leu	Lys	Phe	Gln	Asn	Thr
			805						810					815	
Ser	Leu	Lys	Asn	Phe	Ala	Leu	Met	Gln	Asn	Met	Val	Asn	Leu	Ile	Asn
			820					825					830		
Thr	Ile	Pro	Ser	Leu	Ile	Val	Phe	Arg	Asn	Pro	His	Leu	Gly	Ala	Asn
		835					840					845			
Gly	Tyr	Gln	Ile	Lys	Thr	Gly	Ser	Val	Val	Phe	Gly	Ile	Thr	Lys	Glu
	850					855					860				
Tyr	Leu	Gly	Leu	Glu	Lys	Ile	Asp	Leu	Val	Gly	Lys	Thr	Leu	Asp	Ile
865					870					875					880
Ala	Gly	Asn	Gly	Ile	Ile	Glu	Leu	Asp	Lys	Asn	Lys	Leu	Asp	Leu	Asn
			885						890					895	
Leu	Glu	Val	Ser	Thr	Ile	Lys	Ala	Leu	Ser	Asn	Val	Leu	Asn	Lys	Ile
			900					905					910		
Pro	Ile	Val	Gly	Tyr	Leu	Val	Leu	Gly	Lys	Gly	Gly	Lys	Ile	Thr	Thr
		915					920					925			
Asn	Val	Asn	Val	Lys	Gly	Thr	Leu	Asp	Lys	Pro	Lys	Thr	Gln	Val	Thr
	930					935					940				
Leu	Ala	Ser	Asp	Ile	Ile	Gln	Ala	Pro	Phe	Lys	Ile	Leu	Arg	Arg	Ile
945					950					955					960
Phe	Thr	Pro	Ile	Asp	Ile	Ile	Val	Asp	Glu	Val	Lys	Lys	Asn	Ile	Asp
			965						970					975	
Ser	Lys	Arg	Lys	Leu	Lys										

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(2) INFORMATION FOR SEQ ID NO:1845:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 371 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1845

```

Arg Pro Phe Arg Ser Leu Ile Arg Ile Thr His Ala Pro Lys Leu Lys
1      5      10      15
Pro Ser Phe Ala Leu Glu Cys Val Ile Thr Trp Glu Ala Ile Asn Ser
      20      25      30
Met Glu Ile Thr Leu Phe Asp Pro Ile Asp Ala His Leu His Val Arg
      35      40      45
Glu Asn Ala Leu Leu Lys Ala Val Leu Glu Tyr Ser Ser Glu Pro Phe
      50      55      60
Ser Ala Ala Val Ile Met Pro Asn Leu Ser Lys Pro Leu Ile Asp Thr
      65      70      75      80
Pro Ile Thr Leu Glu Tyr Glu Glu Glu Ile Leu Lys Asn Ser Ser Asn
      85      90      95
Phe Lys Pro Leu Met Ser Leu Tyr Phe Asn Asp Gly Leu Thr Leu Glu
      100     105     110
Glu Leu Gln Arg Ala Lys Asn Lys Gly Ile Lys Phe Leu Lys Leu Tyr
      115     120     125
Pro Lys Gly Met Thr Thr Asn Ala Gln Asn Gly Thr Ser Asp Leu Leu
      130     135     140
Gly Glu Lys Thr Leu Glu Val Leu Glu Asn Ala Gln Lys Leu Gly Phe
      145     150     155     160
Ile Leu Cys Val His Ala Glu Gln Ala Gly Phe Cys Leu Asp Lys Glu
      165     170     175
Phe Leu Cys His Ser Val Leu Glu Thr Phe Ala Leu Ser Phe Pro Lys
      180     185     190
Leu Lys Ile Ile Ile Glu His Leu Ser Asp Trp Arg Ser Ile Ala Leu
      195     200     205
Ile Glu Lys His Asp Asn Leu Tyr Ala Thr Leu Thr Leu His His Ile
      210     215     220
Ser Met Thr Leu Asp Asp Leu Leu Gly Gly Ser Leu Asp Pro His Cys
      225     230     235     240
Phe Cys Lys Pro Leu Ile Lys Thr Lys Lys Asp Gln Glu Arg Leu Leu
      245     250     255
Ser Leu Ala Leu Lys Ala His Pro Lys Ile Ser Phe Gly Ser Asp Ser
      260     265     270
Ala Pro His Phe Ile Ser Lys Lys His Ser Ala Asn Ile Pro Ala Gly
      275     280     285
Ile Phe Ser Ala Pro Ile Leu Leu Pro Ala Leu Cys Glu Leu Phe Glu
      290     295     300
Lys His Asn Ala Leu Glu Asn Leu Gln Ala Phe Ile Ser Asp Asn Ala
      305     310     315     320
Lys Lys Ile Tyr Ala Leu Asp Asn Leu Pro Ser Lys Lys Ala His Leu
      325     330     335

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```

Ser Lys Lys Pro Phe Ile Val Pro Thr His Thr Leu Cys Leu Asn Glu
      340      345      350
Lys Ile Ala Ile Leu Arg Gly Gly Glu Thr Leu Ser Trp Asn Leu Gln
      355      360      365
Glu Ile Ala
      370

```

(2) INFORMATION FOR SEQ ID NO:1846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1846

```

Glu Ile Tyr Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly
1      5      10      15
Lys Asn Phe Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser
      20      25      30
Leu Ile Leu Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu
      35      40      45
His Arg Glu Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn
      50      55      60
Pro Glu Asn Leu Leu Val Leu Lys Arg Gly His Ser Gln Asp Pro Ser
      65      70      75      80
Lys Asn Asn Pro Gly Ala Pro Lys Pro Thr Leu Ala Gly Pro Gln Lys
      85      90      95
Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Thr Pro Pro Lys Pro
      100      105      110
Ile Glu Lys Pro Lys Pro Glu Pro Lys Pro Lys Pro Lys Pro Glu Pro
      115      120      125
Lys Lys Pro Asn His Lys His Lys Ala Leu Lys Lys Val Glu Lys Val
      130      135      140
Glu Glu Lys Lys Val Val Glu Glu Lys Lys Glu Lys Lys Val Val
      145      150      155      160
Glu Gln Lys Val Glu Gln Lys Lys Ile Glu Glu Lys Lys Pro Val Lys
      165      170      175
Lys Glu Phe Asp Pro Asn Gln Leu Ser Phe Leu Pro Lys Glu Val Ala
      180      185      190
Pro Pro Arg Gln Glu Asn Asn Lys Gly Leu Asp Asn Gln Thr Arg Arg
      195      200      205
Asp Ile Asp Glu Leu Tyr Gly Glu Glu Phe Gly Asp Leu Gly Thr Ala
      210      215      220
Arg Lys Arg Phe His Gln Glu
      225      230

```

(2) INFORMATION FOR SEQ ID NO:1847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid

1374

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...206

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1847

```

Ser Arg Tyr His Pro Arg Gly Phe Ser Gln Leu Pro Lys Leu Lys Leu
1      5      10      15
Ile Cys Ile Thr Ala Thr Gly Thr Asp Asn Val Asp Ile Lys Ser Ala
20     25     30
Lys Ala Leu Gly Ile Glu Val Lys Asn Val Ser Ala Tyr Ser Thr Glu
35     40     45
Ser Val Ala Gln His Thr Leu Ala Cys Ala Leu Ser Leu Leu Gly Arg
50     55     60
Ile Asn Asp Tyr Asp Arg Tyr Cys Lys Ser Gly Glu Tyr Ser Gln Ser
65     70     75     80
Asp Ile Phe Thr His Ile Ser Asp Ile Lys Met Gly Leu Ile Lys Gly
85     90     95
Gly Gln Trp Gly Val Ile Gly Leu Gly Asn Ile Gly Lys Arg Val Ala
100    105    110
Lys Leu Ala Gln Ala Phe Gly Ala Lys Val Val Tyr Phe Ser Pro Lys
115    120    125
Asp Lys Lys Glu Glu Tyr Glu Arg Leu Ser Leu Glu Glu Leu Leu Lys
130    135    140
Thr Ser Gly Ile Ile Ser Ile His Ala Pro Leu Asn Glu Ser Thr Arg
145    150    155    160
Asp Leu Ile Ala Leu Lys Glu Leu Gln Ser Leu Lys Asp Gly Ala Ile
165    170    175
Leu Ile Asn Val Gly Arg Gly Gly Ile Val Asn Glu Lys Asp Leu Ala
180    185    190
Leu Ile Leu Glu Thr Lys Asp Leu Tyr Tyr Ala Ser Asp Val
195    200    205

```

(2) INFORMATION FOR SEQ ID NO:1848:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1848

```

Ile Leu Glu Asn Leu Arg Ile Tyr Ala Arg Leu Leu Glu Met Ile Leu
1      5      10      15

```

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```

Lys Asn Leu Ile Leu Leu Phe Leu Ala Lys Arg Lys Leu Ile Phe Ile
      20      25      30
Glu Ala Asn Phe Tyr Thr Ile Ser Gly Ser Lys Leu Asn Glu Val Ala
      35      40      45
Arg Ser Tyr Gln Asp Leu Ala Leu Lys Phe Glu Ala Phe Pro Asn Tyr
      50      55      60
Glu Phe Ile Trp Ile Thr Asp Gly Ile Gly Trp Leu Asp Ala Lys Ser
      65      70      75      80
Lys Leu Gln Glu Ala Tyr Lys Ser Val Glu Ile Tyr Asn Leu Ser Tyr
      85      90      95
Val Asn Asp Phe Ile Ser Lys Val Gln Lys
      100      105

```

(2) INFORMATION FOR SEQ ID NO:1849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1849

```

Cys Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys
1      5      10      15
Met Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln
      20      25      30
Ile Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly
      35      40      45
Ile Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys
      50      55      60
Ala Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn
      65      70      75      80
Phe Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala
      85      90      95
Phe Gly Asn Asp Thr Lys Lys Phe Asp Phe Val Ile Phe Ser Lys Glu
      100      105      110
Lys Thr Tyr Phe His Arg Ser
      115

```

(2) INFORMATION FOR SEQ ID NO:1850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1850

```

Leu Val Ile Asn Ser Lys Thr Gly Leu Leu Thr Ile Lys Gly Glu Asp
1      5      10      15
Ala Leu Gly Lys Ala Ser Leu Lys Asp Leu Gly Leu Ser Ala Gly Met
20     25     30
Val Gln Ser Tyr Glu Ala Ser Gln Asp Thr Leu Phe Met Ser Lys Asn
35     40     45
Leu Gln Lys Ala Ser Asp Ser Gln Phe Thr Tyr Asn Gly Val Ser Ile
50     55     60
Thr Arg Pro Thr Asn Glu Val Asn Asp Val Ile Ser Gly Val Asn Ile
65     70     75     80
Thr Leu Glu Gln Thr Thr Glu Pro Asn Lys Pro Ala Ile Ile Ser Val
85     90     95
Ser Arg Asp Asn Gln Ala Ile Ile Asp Ser Leu Lys Glu Phe Val Lys
100    105    110
Ala Tyr Asn Glu Leu Ile Pro Lys Leu Asp Glu Asp Thr Arg Tyr Asp
115    120    125
Ala Asp Thr Lys Ile Ala Gly Ile Phe Asn Gly Val Gly Asp Ile Arg
130    135    140
Ala Ile Arg Ser Ser Leu Asn Asn Val Phe Ser Tyr Ser Val His Thr
145    150    155    160
Asp Asn Gly Val Glu Ser Leu Met Lys Tyr Gly Leu Ser Leu Asp Asp
165    170    175
Lys Gly Val Met Ser Leu Asp Glu Ala Lys Leu Ser Ser Ala Leu Asn
180    185    190
Ser Asn Pro Lys Ala Thr Gln Asp Phe Phe Tyr Gly Ser Asp Ser Lys
195    200    205
Asp Met Gly Gly Arg Glu Ile His Gln Glu Gly Ile Phe Ser Lys Phe
210    215    220
Asn Gln Val Ile Ala Asn Leu Ile Asp Gly Gly Asn Ala Lys Leu Lys
225    230    235    240
Ile Tyr Glu Asp Ser Leu Asp Arg Asp Ala Lys Ser Leu Thr Lys Asp
245    250    255
Lys Glu Asn Ala Gln Glu Leu Leu Lys Thr Arg Tyr Asn Ile Met Ala
260    265    270
Glu Arg Phe Ala Ala Tyr Asp Ser Gln Ile Ser Lys Ala Asn Gln Lys
275    280    285
Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala Lys Lys Asn
290    295    300

```

(2) INFORMATION FOR SEQ ID NO:1851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...129

1377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1851

```

Arg Asn Ile Met Gln Tyr Ala Asn Ala Tyr Gln Ala Tyr Gln His Asn
1           5           10           15
Arg Val Ser Val Glu Ser Pro Ala Lys Leu Ile Glu Met Leu Tyr Glu
          20           25           30
Gly Ile Leu Arg Phe Ser Ser Gln Ala Lys Arg Cys Ile Glu Asn Glu
          35           40           45
Asp Ile Glu Lys Lys Ile Tyr Tyr Ile Asn Arg Val Thr Asp Ile Phe
          50           55           60
Thr Glu Leu Leu Asn Ile Leu Asp Tyr Glu Lys Gly Gly Lys Val Ala
          65           70           75           80
Val Tyr Leu Thr Gly Leu Tyr Thr His Gln Ile Lys Val Leu Thr Gln
          85           90           95
Ala Asn Val Glu Asn Asp Ala Ser Lys Ile Asp Leu Val Leu Asn Val
          100          105          110
Ala Arg Gly Leu Leu Glu Ala Trp Arg Glu Ile His Ser Asp Glu Leu
          115          120          125
Ala

```

(2) INFORMATION FOR SEQ ID NO:1852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1852

```

Phe Asp Asp Leu Tyr Gly Ser Asn Ser Leu Pro Phe Tyr Pro Arg Val
1           5           10           15
Thr Pro Val Lys Phe Pro Thr Phe Lys Trp Ala Leu Leu Lys Ala Leu
          20           25           30
Ile Lys Asp Asp Phe Pro Thr Leu Gly Trp Pro Thr Arg Ala Thr Met
          35           40           45
Ile Ser Phe Ile Gly Phe Glu Cys Ser Ala Leu Lys Val Phe Leu Ile
          50           55           60
Phe Gly Tyr Ile Val Phe Lys Ser Trp His Tyr Ser Ala Ile Arg Leu
          65           70           75           80
Ile Val Ile

```

(2) INFORMATION FOR SEQ ID NO:1853:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1378

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1853

```

Lys Arg Asp Lys Asn Val Lys Met Arg Lys Gly Arg Val Met Leu Cys
1      5      10      15
Val Phe Asp Ile Glu Thr Ile Pro Asn Ile Ser Leu Cys Lys Glu His
20      25      30
Phe Gln Leu Lys Glu Asp Asp Ala Leu Lys Ile Cys Glu Trp Ser Phe
35      40      45
Glu Lys Gln Lys Glu Lys Ser Gly Ser Glu Phe Leu Pro Leu Tyr Leu
50      55      60
His Glu Ile Ile Ser Ile Ala Ala Val Ile Gly Asp Asp Tyr Gly Gln
65      70      75      80
Phe Ile Lys Val Gly Asn Phe Gly Gln Lys His Glu Asn Lys Glu Asp
85      90      95
Phe Ala Ser Glu Lys Glu Leu Leu Glu Asp Phe Phe Lys Tyr Phe Asn
100     105     110
Glu Lys Gln Pro Arg Leu Ile Ser Phe Asn Gly Arg Gly Phe Asp Ile
115     120     125
Pro Leu Leu Thr Leu Lys Ala Leu Lys Tyr Asn Leu Thr Leu Asp Ala
130     135     140
Phe Tyr Ser Gln Glu Asn Lys Trp Glu Asn Tyr Arg Ala Arg Tyr Ser
145     150     155     160
Glu Gln Phe His Leu Asp Leu Met Asp Ser Leu Ser His Tyr Gly Ser
165     170     175
Val Arg Gly Leu Asn Leu Asn Gly Val Cys Ser Met Thr Asn Ile Pro
180     185     190
Gly Lys Phe Asp Val Ser Gly Asp Leu Val His Ala Ile Tyr Tyr Asn
195     200     205
Pro His Leu Arg Pro Lys Gly Gly Lys Arg His Tyr
210     215     220

```

(2) INFORMATION FOR SEQ ID NO:1854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...254

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1854

```

Arg Phe Lys Ala Arg Ile Val Arg Phe Phe Ile Phe Leu Ile Leu Ile
1      5      10      15
Cys Pro Leu Ile Cys Pro Leu Met Ser Ala Asp Ser Ala Leu Pro Ser
20      25      30

```


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```

Val Asn Leu Ser Leu Asn Ala Pro Ser Asp Pro Lys Gln Leu Val Thr
    35          40          45
Thr Leu Asn Val Ile Ala Leu Thr Leu Leu Val Leu Ala Pro Ser
    50          55          60
Leu Ile Leu Val Met Thr Ser Phe Thr Arg Leu Ile Val Val Phe Ser
    65          70          75          80
Phe Leu Arg Thr Ala Leu Gly Thr Gln Gln Thr Pro Pro Thr Gln Ile
    85          90          95
Leu Val Ser Leu Ser Leu Ile Leu Thr Phe Phe Ile Met Glu Pro Ser
    100         105         110
Leu Lys Lys Ala Tyr Asp Thr Gly Ile Lys Pro Tyr Met Asp Lys Lys
    115         120         125
Ile Ser Tyr Thr Glu Ala Phe Glu Lys Ser Thr Leu Pro Phe Lys Glu
    130         135         140
Phe Met Leu Lys Asn Thr Arg Glu Lys Asp Leu Ala Leu Phe Phe Arg
    145         150         155         160
Ile Arg Asn Leu Pro Asn Pro Lys Thr Pro Asp Asp Val Ser Leu Ser
    165         170         175
Val Leu Ile Pro Ala Phe Met Ile Ser Glu Leu Lys Thr Ala Phe Gln
    180         185         190
Ile Gly Phe Leu Leu Tyr Leu Pro Phe Leu Val Ile Asp Met Val Ile
    195         200         205
Ser Ser Ile Leu Met Ala Met Gly Met Met Met Leu Pro Pro Val Met
    210         215         220
Ile Ser Leu Pro Phe Lys Ile Leu Val Phe Ile Leu Val Asp Gly Phe
    225         230         235         240
Asn Leu Leu Thr Glu Asn Leu Val Ala Ser Phe Lys Met Val
    245         250

```

(2) INFORMATION FOR SEQ ID NO:1855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...614

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1855

```

Lys Trp Gly Ile Leu Pro Gly Leu Pro Val Asp Lys Met Glu Val Ser
1      5      10      15
Leu Ile His Lys Asp His Gln Ile Thr Ile Ile Asp Leu Pro Gly Thr
    20      25      30
Tyr Ala Leu Asn Asp Phe Thr Thr Glu Glu Lys Val Thr Lys Asp Phe
    35      40      45
Leu Glu Lys Gly Gln Tyr Asn Leu Ile Leu Asn Val Val Asp Ser Thr
    50      55      60
Asn Leu Glu Arg Asn Leu Ala Leu Ser Ala Gln Leu Leu Asp Thr Asn
    65      70      75      80
Lys Lys Met Leu Leu Ala Leu Asn Met Trp Asp Glu Ala Lys Lys Glu
    85      90      95
Gly Ile Asn Ile Asn Thr Glu Lys Leu Ser Gln Glu Leu Gly Val Val
    100     105     110
Cys Val Pro Thr Ser Ala Arg Ser Lys Glu Asp Arg Leu Asn Thr Glu

```

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115	120	125
Leu Leu Leu Asp Glu Ile Val Arg Leu Tyr Ser Gln Asn Thr Thr Asn		
130	135	140
Asn Glu Asn Ile Lys Val Pro Ser Gln Ser Phe Lys Glu Ser Leu Lys		
145	150	155
Tyr Ser Gln Ser Ala Gln Arg Ile Ala Lys Ser Val Ile Ser Glu Asn		
165	170	175
Lys Gln Asn Ala Ser Phe Glu His Thr Tyr Lys Ile Asp Lys Ile Leu		
180	185	190
Met His Gln Arg Tyr Gly Ile Phe Ile Phe Leu Gly Phe Met Phe Ile		
195	200	205
Ile Phe Ser Leu Ser Phe Leu Ile Gly Gly Gly Val Gln Lys Ala Leu		
210	215	220
Glu Glu Gly Phe Lys Ile Leu Ser Asp Ser Ile Lys Glu Asn Val Ala		
225	230	235
Asn Glu Asp Leu Ala Ser Leu Val Gly Asp Gly Ile Ile Gly Gly Val		
245	250	255
Gly Ala Thr Val Ser Phe Leu Pro Leu Ile Val Val Leu Tyr Phe Gly		
260	265	270
Ile Ser Leu Glu Thr Thr Gly Tyr Met Ser Arg Val Ala Phe Leu		
275	280	285
Leu Asp Gly Ile Leu His Lys Phe Gly Leu His Gly Lys Ser Phe Ile		
290	295	300
Pro Leu Ile Thr Gly Phe Gly Cys Ser Val Pro Ala Tyr Met Ala Thr		
305	310	315
Arg Thr Leu Gln Asn Tyr Asn Glu Arg Leu Ile Thr Leu Phe Val Ile		
325	330	335
Gly Phe Met Ser Cys Ser Ala Arg Leu Pro Ile Tyr Val Leu Phe Val		
340	345	350
Gly Ser Phe Phe Pro Ser Ser Ser Ala Gly Phe Val Leu Phe Cys Ile		
355	360	365
Tyr Ile Leu Gly Ala Val Val Ala Leu Val Met Ala Lys Leu Leu Lys		
370	375	380
Leu Ser Val Phe Lys Gly Gln Thr Glu Ser Phe Ile Met Glu Met Pro		
385	390	395
Lys Tyr Arg Phe Pro Ser Trp Arg Met Val Tyr Phe Ser Ile Tyr Thr		
405	410	415
Lys Ser Leu Ser Tyr Leu Lys Lys Ala Gly Thr Tyr Ile Leu Val Gly		
420	425	430
Ala Ile Leu Ile Trp Phe Met Ser Gln Tyr Pro Lys Asn Asp Ala Ala		
435	440	445
Met Lys Thr Tyr Lys Gln Glu Ser Leu Leu Val Gln Lys Asn Ala Asn		
450	455	460
Leu Ser Ser Glu Ala Lys Glu Glu Lys Leu Lys Glu Leu Lys Thr Glu		
465	470	475
Leu Asp Lys Lys Asn Leu Lys Asn Ser Val Val Gly Arg Gly Gly Ala		
485	490	495
Tyr Leu Glu Lys Val Phe Asn Pro Met Asp Phe Asp Trp Arg Leu Ser		
500	505	510
Val Ser Leu Val Thr Gly Phe Met Ala Lys Glu Val Val Val Ser Thr		
515	520	525
Leu Gly Val Leu Phe Ser Leu Gly Asp Gln Asn Glu Lys Ser Asp Ala		
530	535	540
Phe Arg Glu Ile Ile Arg Lys Glu Val Ser Val Pro Ser Gly Ile Ala		
545	550	555
Phe Ile Val Phe Val Met Phe Tyr Ile Pro Cys Phe Ala Ala Thr Ile		
565	570	575
Thr Phe Gly Arg Glu Ala Gly Gly Ile Lys Phe Val Ala Tyr Leu Phe		
580	585	590
Ile Phe Thr Thr Val Val Ala Tyr Ala Phe Ser Leu Ile Ala Phe Tyr		
595	600	605
Ala Thr Gln Ile Leu Val		
610		

1381

(2) INFORMATION FOR SEQ ID NO:1856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1856

```

Met Lys Arg Ile Leu Val Ser Leu Ala Val Leu Ser His Ser Ala His
1      5      10      15
Ala Val Lys Thr His Asn Leu Glu Arg Val Glu Ala Ser Gly Val Ala
20     25     30
Asn Asp Lys Glu Ala Pro Leu Ser Trp Arg Ser Lys Glu Val Arg Asn
35     40     45
Tyr Met Gly Ser Arg Thr Val Ile Ser Asn Lys Gln Leu Thr Lys Ser
50     55     60
Ala Asn Gln Ser Ile Glu Glu Ala Leu Gln Asn Val Pro Gly Val His
65     70     75     80
Ile Arg Asn Ser Thr Gly Ile Gly Ala Val Pro Ser Ile Ser Ile Arg
85     90     95
Gly Phe Gly Ala Gly Gly Pro Gly His Ser Asn Thr Gly Met Ile Leu
100    105    110
Val Asn Gly Ile Pro Ile Tyr Val Ala Pro Tyr Val Glu Ile Gly Thr
115    120    125
Val Ile Phe Pro Val Thr Phe Gln Ser Val Asp Arg Ile Ser Val Thr
130    135    140
Lys Gly Gly Glu Ser Val Arg Tyr Gly Pro Asn Ala Phe Gly Gly Val
145    150    155    160
Ile Asn Ile Ile Thr Lys Gly Ile Pro Thr Asn Trp Glu Ser Gln Val
165    170    175
Ser Glu Arg Thr Thr Phe Trp Gly Lys Ser Glu Asn Gly Gly Phe Phe
180    185    190
Asn Gln Asn Ser Lys Asn Ile Asp Lys Ser Leu Val Asn Asn Met Leu
195    200    205
Phe Asn Thr Tyr Leu Arg Thr Gly Gly Met Met Asn Lys His Phe Gly
210    215    220
Ile Gln Ala Gln Val Asn Trp Leu Lys Gly Gln Gly Phe Arg Tyr Asn
225    230    235    240
Ser Pro Thr Asp Ile Gln Asn Tyr Met Leu Asp Ser Leu Tyr Gln Ile
245    250    255
Asn Asp Ser Asn Lys Ile Thr Ala Phe Phe Gln Tyr Tyr Ser Tyr Phe
260    265    270
Leu Thr Asp Pro Gly Ser Leu Gly Ile Ala Ala Tyr Asn Gln Asn Arg
275    280    285
Phe Gln Asn Asn Arg Pro Asn Asn Asp Lys Ser Gly Arg Ala Lys Arg
290    295    300
Trp Gly Ala Val Tyr Gln Asn Phe Phe Gly Asp Thr Asp Arg Val Gly
305    310    315    320
Gly Gly Phe His Phe
325

```

(2) INFORMATION FOR SEQ ID NO:1857:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...797

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1857

```

Arg Leu Lys Pro Asn Val Ile Glu Arg Arg Met Leu Glu Lys Leu Leu
1      5      10      15
Ser Ala Ile Lys Gln Lys Val Ser Asn Tyr Phe Leu Gly Val Leu Pro
      20      25      30
Lys Ser Tyr Ser Met Ser Glu Glu Asn Asn Ile Leu Gly Leu Tyr Asp
      35      40      45
Glu His Phe Leu Leu Thr Lys Asn Glu Asn Leu Val Gly Ile Leu Arg
      50      55      60
Leu Glu Gly Val Ser Tyr Thr His Leu Ser Thr Glu Gln Leu Gln Asp
      65      70      75      80
Leu Phe Thr Glu Arg Gln Met Ala Leu Asp Ser Leu Glu Lys Val Val
      85      90      95
Ala Arg Leu Val Val Lys Arg Arg Lys Ile Asp Tyr Lys Gln Ser Ile
      100     105     110
Gln Ser Asp Ser Gln Tyr Leu Gln Ala Ile Leu Asn Gln Phe Glu Asn
      115     120     125
Lys Glu Val Tyr Glu Asn Gln Tyr Phe Leu Val Leu Glu Ser Thr His
      130     135     140
Ser Leu His Gly Val Leu Glu His Lys Lys Lys Ser Phe Met His Ala
      145     150     155     160
Asn Arg Glu Asn Phe Lys Asp Ile Leu Ser Tyr Lys Ala His Phe Leu
      165     170     175
Gln Glu Thr Leu Lys Ser Leu Glu Ile Gln Leu Lys Asn Tyr Ala Pro
      180     185     190
Lys Leu Leu Asn Ser Lys Glu Val Leu Asn Phe Tyr Ala Glu Tyr Ile
      195     200     205
Asn Gly Phe Glu Leu Pro Leu Lys Pro Leu Val Gly Gly Tyr Leu Ser
      210     215     220
Asp Ser Tyr Ile Ala Ser Ser Ile Thr Phe Glu Lys Asp Tyr Phe Ile
      225     230     235     240
Gln Glu Ser Phe Asn Gln Lys Thr Tyr Asn Arg Leu Ile Gly Ile Lys
      245     250     255
Ala Tyr Glu Ser Glu Arg Ile Thr Ser Ile Ala Val Gly Ala Leu Leu
      260     265     270
Tyr Gln Glu Thr Pro Leu Asp Ile Ile Phe Ser Ile Glu Pro Met Ser
      275     280     285
Val Asn Lys Thr Leu Ser Phe Leu Lys Glu Arg Ala Lys Phe Ser Met
      290     295     300
Ser Asn Leu Val Lys Asn Glu Leu Leu Glu Tyr Gln Glu Leu Val Lys
      305     310     315     320
Thr Lys Arg Leu Ser Met Gln Lys Phe Ala Leu Asn Val Leu Ile Lys
      325     330     335
Ala Pro Ser Leu Glu Asp Leu Asp Ala Gln Thr Ser Leu Ile Leu Gly
      340     345     350
Leu Leu Phe Lys Glu Asn Leu Val Gly Val Ile Glu Thr Phe Gly Leu
      355     360     365

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Lys Gly Gly Tyr Phe Ser Phe Phe Pro Glu Arg Ile His Leu Asn His
 370 375 380
 Arg Leu Arg Phe Leu Thr Ser Lys Ala Leu Ala Cys Leu Met Val Phe
 385 390 395 400
 Glu Arg Gln Asn Leu Gly Phe Lys Ala Asn Ser Trp Gly Asn Ser Pro
 405 410 415
 Leu Ser Val Phe Lys Asn Leu Asp Tyr Ser Pro Phe Leu Phe Asn Phe
 420 425 430
 His Asn Gln Glu Val Ser His Asn Asn Ala Lys Glu Ile Ala Arg Val
 435 440 445
 Asn Gly His Thr Leu Val Ile Gly Ala Thr Gly Ser Gly Lys Ser Thr
 450 455 460
 Leu Ile Ser Tyr Leu Met Met Ser Ala Leu Lys Tyr Gln Asn Met Arg
 465 470 475 480
 Leu Leu Ala Phe Asp Arg Met Gln Gly Leu Tyr Ser Phe Thr Glu Phe
 485 490 495
 Phe Lys Gly His Tyr His Asp Gly Gln Ser Phe Ser Ile Asn Pro Phe
 500 505 510
 Cys Leu Glu Pro Asn Leu Gln Asn Leu Glu Phe Leu Gln Ser Phe Phe
 515 520 525
 Leu Ser Met Leu Asp Leu Ala Pro Ser Arg Asp Lys Glu Ala Leu Glu
 530 535 540
 Asp Met Asn Ala Ile Ser Gly Ala Ile Lys Ser Leu Tyr Glu Thr Leu
 545 550 555 560
 Tyr Pro Lys Asp Phe Ser Leu Leu Asp Phe Lys Glu Thr Leu Lys Arg
 565 570 575
 Thr Ser Ser Asn Gln Leu Gly Leu Ser Leu Glu Pro Tyr Leu Asn Asn
 580 585 590
 Pro Leu Phe Asn Ala Leu Asn Asp Ala Phe Asn Ser Asn Ala Phe Leu
 595 600 605
 Asn Val Ile Asn Leu Asp Ala Ile Thr Gln Asn Pro Lys Asp Leu Gly
 610 615 620
 Leu Leu Ala Tyr Tyr Leu Phe Tyr Lys Ile Leu Glu Glu Ser Arg Lys
 625 630 635 640
 Asn Asp Ser Gly Phe Leu Val Phe Leu Asp Glu Phe Lys Ser Tyr Val
 645 650 655
 Glu Asn Asp Leu Leu Asn Thr Lys Ile Asn Ala Leu Ile Thr Gln Ala
 660 665 670
 Arg Lys Ala Asn Gly Val Val Val Leu Ala Leu Gln Asp Ile Tyr Gln
 675 680 685
 Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly Thr
 690 695 700
 Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn Phe
 705 710 715 720
 Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr Pro
 725 730 735
 Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser Ser
 740 745 750
 Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys Ile
 755 760 765
 Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln Lys
 770 775 780
 Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
 785 790 795

(2) INFORMATION FOR SEQ ID NO:1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 529 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1858

```

Lys Met Ile Leu Lys Ser Ser Ile Asp Arg Leu Leu Gln Thr Ile Asp
1      5      10      15
Ile Val Glu Val Ile Ser Ser Tyr Val Asp Leu Arg Lys Ser Gly Ser
20      25      30
Asn Tyr Met Ala Cys Cys Pro Phe His Glu Glu Arg Ser Ala Ser Phe
35      40      45
Ser Val Asn Gln Val Lys Gly Phe Tyr Tyr Cys Phe Gly Cys Gly Ala
50      55      60
Ser Gly Asp Ser Ile Lys Phe Val Met Ala Phe Glu Lys Leu Ser Phe
65      70      75      80
Val Glu Ala Leu Glu Lys Leu Ala His Arg Phe Asn Ile Ala Leu Glu
85      90      95
Tyr Asp Lys Gly Val Tyr Tyr Asp His Lys Glu Asp Tyr His Leu Leu
100     105     110
Glu Met Val Ser Ser Leu Tyr Gln Glu Glu Leu Phe Asn Ala Pro Phe
115     120     125
Phe Leu Asn Tyr Leu Gln Lys Arg Gly Leu Ser Met Glu Ser Ile Lys
130     135     140
Ala Phe Lys Leu Gly Leu Cys Thr Asn Lys Ile Asp Tyr Gly Ile Glu
145     150     155     160
Asn Lys Gly Leu Asn Lys Asp Lys Leu Ile Glu Leu Gly Val Leu Gly
165     170     175
Lys Ser Asp Lys Glu Asp Lys Thr Tyr Leu Arg Phe Leu Asp Arg Ile
180     185     190
Met Phe Pro Ile Tyr Ser Pro Ser Ala Gln Val Val Gly Phe Gly Gly
195     200     205
Arg Thr Leu Lys Glu Lys Ala Ala Lys Tyr Ile Asn Ser Pro Gln Asn
210     215     220
Lys Leu Phe Asp Lys Ser Ser Leu Leu Tyr Gly Tyr His Leu Ala Lys
225     230     235     240
Glu His Ile Tyr Lys Gln Lys Gln Val Ile Val Thr Glu Gly Tyr Leu
245     250     255
Asp Val Ile Leu Leu His Gln Ala Gly Phe Lys Asn Ala Ile Ala Thr
260     265     270
Leu Gly Thr Ala Leu Thr Pro Ser His Leu Pro Leu Leu Lys Lys Gly
275     280     285
Asp Pro Glu Ile Leu Leu Ser Tyr Asp Gly Asp Lys Ala Gly Arg Asn
290     295     300
Ala Ala Tyr Lys Ala Ser Leu Met Leu Ala Lys Glu Gln Arg Lys Gly
305     310     315     320
Gly Val Ile Leu Phe Glu Asn Asn Leu Asp Pro Ala Asp Met Ile Ala
325     330     335
Asn His Gln Ile Glu Thr Leu Lys Asn Trp Leu Ser Arg Pro Ile Ala
340     345     350
Phe Ile Glu Phe Val Leu Arg His Met Ala Gly Ser Tyr Leu Leu Asp
355     360     365
Asp Pro Leu Glu Lys Asp Lys Ala Leu Lys Glu Met Leu Gly Phe Leu
370     375     380
Lys Asn Phe Ser Leu Leu Leu Gln Asn Glu Tyr Lys Pro Leu Ile Ala
385     390     395     400
Thr Leu Leu Gln Ala Pro Leu His Val Leu Gly Ile Arg Glu Pro Val
405     410     415
Ser Phe Gln Pro Phe Tyr Pro Lys Thr Glu Lys Pro Asn Arg Pro Gln
420     425     430

```

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```

Lys Phe Ala His Val Ser Ser Met Pro Ser Leu Glu Phe Leu Glu
    435                      440                      445
Leu Val Ile Arg Tyr Leu Leu Glu Asp Arg Ser Leu Leu Asp Leu Ala
    450                      455                      460
Val Gly Tyr Ile His Ser Gly Val Phe Leu His Lys Lys Gln Glu Phe
    465                      470                      475                      480
Asp Ala Leu Cys Gln Glu Lys Leu Asp Asp Pro Lys Leu Val Ala Leu
    485                      490                      495
Leu Leu Asp Ala Asn Leu Pro Leu Lys Lys Gly Gly Phe Glu Lys Glu
    500                      505                      510
Leu Arg Leu Leu Ile Leu Arg Tyr Phe Glu Pro Pro Thr Gln Arg Asn
    515                      520                      525
Pro

```

(2) INFORMATION FOR SEQ ID NO:1859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...430

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1859

```

Leu Arg Gly His Arg Arg Thr Tyr Ile Gly Ser Met Pro Gly Arg Ile
1          5          10          15
Val Gln Gly Leu Ile Glu Ala Lys Lys Met Asn Pro Val Met Val Leu
    20          25          30
Asp Glu Ile Asp Lys Val Asp Arg Ser Val Arg Gly Asp Pro Ala Ser
    35          40          45
Ala Leu Leu Glu Ile Leu Asp Pro Glu Gln Asn Ile Ala Phe Arg Asp
    50          55          60
His Tyr Ala Asn Phe Ser Ile Asp Leu Ser Gln Val Ile Phe Ile Ala
    65          70          75          80
Thr Ala Asn Asn Ile Asp Arg Ile Pro Ala Pro Leu Arg Asp Arg Met
    85          90          95
Glu Phe Ile Ser Val Ser Ser Tyr Thr Pro Ser Glu Lys Glu Glu Ile
    100         105         110
Ala Lys Asn Tyr Leu Ile Pro Gln Glu Leu Glu Lys His Ala Leu Lys
    115         120         125
Pro Ser Glu Val Asp Ile Ser His Glu Cys Leu Lys Leu Ile Ile Glu
    130         135         140
Lys Tyr Thr Arg Glu Ala Gly Val Arg Asp Leu Arg Arg Gln Ile Ala
    145         150         155         160
Thr Ile Met Arg Lys Ala Ala Leu Lys Tyr Leu Glu Asp Asn Pro His
    165         170         175
Lys Lys Gly Arg Thr Lys Lys Ser Glu Asp Lys Asp Lys Lys Gly Gly
    180         185         190
Asn Glu Glu Asn Glu Lys Arg Gly Glu Ser Lys Asp Phe Cys Val Ser
    195         200         205
Ile Thr Pro Asp Asn Leu Lys Glu Tyr Leu Glu Arg Met Val Phe Glu
    210         215         220
Ile Asp Pro Ile Asp Glu Glu Asn Lys Ile Gly Ile Val Asn Gly Leu

```

```

225          230          235          240
Ala Trp Thr Pro Val Gly Gly Asp Val Leu Lys Ile Glu Ala Val Lys
          245          250          255
Ile Arg Gly Lys Gly Glu Leu Lys Leu Thr Gly Ser Leu Gly Asp Val
          260          265          270
Met Lys Glu Ser Ala Ile Ile Ala Phe Ser Val Val Lys Val Leu Leu
          275          280          285
Asp Asn Glu Thr Leu Lys Val Pro Lys Ile Pro Ser Glu Thr Asp Ala
          290          295          300
Glu Asn Lys Lys Lys Lys Val Leu Lys Val Tyr Asn Ala Tyr Asp
305          310          315          320
Leu His Leu His Val Pro Glu Gly Ala Thr Pro Lys Asp Gly Pro Ser
          325          330          335
Ala Gly Ile Ala Met Ala Ser Val Met Ala Ser Ile Leu Cys Asp Arg
          340          345          350
Ala Ile Arg Ser Glu Val Ala Met Thr Gly Glu Leu Thr Leu Ser Gly
          355          360          365
Glu Val Leu Pro Ile Gly Gly Leu Lys Glu Lys Leu Ile Ala Ala Phe
          370          375          380
Lys Ala Gly Ile Lys Thr Ala Leu Ile Pro Val Lys Asn Tyr Glu Arg
385          390          395          400
Asp Leu Asp Glu Ile Pro Thr Glu Val Arg Glu Asn Leu Asn Ile Val
          405          410          415
Ala Val Lys Asn Ile Ala Glu Val Leu Glu Lys Thr Leu Leu
          420          425          430

```

(2) INFORMATION FOR SEQ ID NO:1860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1860

```

Lys Arg Tyr Arg Lys Thr Ala Leu Leu Arg Leu Asp Asn Gly Asp Lys
1          5          10          15
Leu Ser Leu Met Arg Glu Phe Phe Lys Ser Val Arg Gly Phe Leu Asn
          20          25          30
Leu Leu Arg Met Ile Phe Pro Glu Arg Phe Gln Asn Ala Phe Leu Gly
          35          40          45
Leu Ser Glu Leu Phe Tyr Tyr Ala Ser Ser Leu Ser Phe Tyr Thr Ile
          50          55          60
Leu Ser Leu Ser Pro Ile Leu Leu Phe Val Phe Ser Leu Phe Val Ser
65          70          75          80
His Tyr Leu Gln Ala His Ser Gly Glu Met Glu Ala Leu Ile Phe Pro
          85          90          95
Asn Ala Pro Lys Leu Ile Gly Ala Ile Lys Asp Phe Leu Glu Asn Phe
          100          105          110
Lys Lys Thr Asp Met Thr Leu Gly Thr Leu Glu Glu Val Ser Ile Val
          115          120          125
Val Ala Leu Val Leu Phe Cys Glu Asn Tyr Arg Ser Ile Ala Ser Lys
130          135          140

```


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```

Ile Phe Asp Ala Lys Pro Arg Asp Tyr Ala His Phe Lys Gly Lys Glu
145          150          155          160
Ile Phe Leu Phe Trp Gly Phe Gly Thr Thr Leu Val Phe Leu Phe Ala
          165          170          175
Leu Pro Leu Val Val Phe Phe Asp Ile Lys Ile Gln Val Phe Phe Glu
          180          185          190
Asp Lys Asp Ser Ser Leu Leu His Val Leu Arg Trp Ile Gly Thr Tyr
          195          200          205
Ala Phe Phe Leu Ile Leu Phe Thr Ile Pro Thr Asn Lys Val Phe Lys
210          215          220
His Tyr Phe Trp Val Phe Leu Trp Val Phe Phe Thr Ser Val Ser Trp
225          230          235          240
His Val Leu Lys Trp Ala Ser Thr Leu Phe Met Cys Tyr Thr Asn Pro
          245          250          255
His Leu Leu Met Ser Leu Tyr Gly Ser Arg Phe Pro Phe Cys Gly Phe
          260          265          270

```

(2) INFORMATION FOR SEQ ID NO:1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1861

```

Val Gly Val Val Met Ile Lys Lys Thr Leu Ala Ser Val Leu Leu Gly
1          5          10          15
Leu Ser Leu Met Ser Val Leu Asn Ala Lys Glu Cys Val Ser Pro Ile
          20          25          30
Thr Arg Ser Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu
          35          40          45
Gln Leu Gln Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu
          50          55          60
Lys Leu Val Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu
65          70          75          80
Thr Val Leu Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys
          85          90          95
Ile Lys Tyr Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser
          100          105          110
Leu Thr Leu Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser
          115          120          125
Lys Gly Val Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys
          130          135          140
Ala Phe Thr Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser
145          150          155          160
Glu Glu Ser Val Leu Leu Lys Glu Lys Gly Lys Pro Lys Ala Val Arg
          165          170          175
Arg Glu Leu Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp
          180          185          190
Thr Leu His Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser
          195          200          205
Gln Glu Gln Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr

```

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210 215 220
 Glu Trp Ile Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly
 225 230 235 240
 Pro Ile Lys Ala Trp Gln Asn Lys Lys
 245

(2) INFORMATION FOR SEQ ID NO:1862:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1862

His Asp Lys Lys Phe Asp Leu Leu Gly Gly Val Met Asp Phe Val Gly
 1 5 10 15
 Phe Glu Asp Leu Lys Cys Lys Asp Lys Glu Asn Ser Gln Lys Val Phe
 20 25 30
 Val Ile Arg Asn Asp Lys Leu Gly Asp Phe Ile Leu Val Ile Pro Ala
 35 40 45
 Leu Ile Ala Leu Lys His Ala Phe Leu Glu Lys Gly Val Glu Val Tyr
 50 55 60
 Leu Gly Val Val Val Pro Ser Tyr Thr Thr Pro Ile Ala Leu Glu Phe
 65 70 75 80
 Pro Phe Ile Asp Glu Val Ile Ile Glu Asp Asn His Leu Ala Thr Thr
 85 90 95
 Pro Lys Asn Arg Ser Thr Asp Ala Leu Ile Phe Leu Phe Ser Asn Phe
 100 105 110
 Lys Asn Ala Lys Leu Ala Phe Ser Leu Arg Lys Ser Ile Pro Tyr Ile
 115 120 125
 Leu Ala Pro Lys Thr Lys Ile Tyr Ser Trp Leu Tyr Gln Lys Arg Val
 130 135 140
 Arg Gln Asn Arg Ser Leu Cys Leu Lys Thr Glu Tyr Glu Tyr Asn Leu
 145 150 155 160
 Asp Leu Ile His Ala Phe Cys Lys Asp Tyr Asp Leu Pro Asn Ala Gln
 165 170 175
 Leu Lys Lys Ile Ala Trp Lys Leu Lys Asp Lys Ser Lys Glu Arg Ser
 180 185 190
 Ile Ile Ala Ser Lys Leu Asn Ala Asn Val Asp Leu Leu Trp Ile Gly
 195 200 205
 Val His Met His Ser Gly Gly Ser Ser Pro Val Leu Pro Ala Ser His
 210 215 220
 Phe Ile Glu Leu Ile Ala Ile Leu His Glu Lys Leu Ser Cys Glu Ile
 225 230 235 240
 Ile Leu Ile Cys Gly Pro Gly Glu Arg Lys Ala Thr Glu Glu Leu Leu
 245 250 255
 Lys Glu Val Pro Phe Ala His Leu Tyr Asp Thr Ser His Ser Leu Val
 260 265 270
 Asp Leu Ala Lys Leu Cys Ala Asn Leu Ser Val Cys Ile Gly Asn Ala
 275 280 285
 Ser Gly Pro Leu His Val Asn Ala Leu Phe Asp Asn Gln Ser Ile Gly
 290 295 300

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Phe Tyr Pro Asn Glu Leu Thr Ala Ser Ile Ala Arg Trp Arg Pro Phe
 305 310 315 320
 Asn Glu Gln Phe Leu Gly Ile Thr Pro Pro Asn Gly Ser Asn Asp Met
 325 330 335
 Gly Leu Ile Asp Ile Gln Lys Glu Ser Glu Lys Ile Met Gly Phe Ile
 340 345 350
 Thr Lys Asn Leu Ser His His Met Gln Glu Arg
 355 360

(2) INFORMATION FOR SEQ ID NO:1863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...662

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1863

Gly Asn Thr Ile Ile Lys Met Gln Lys Ser Leu Ile Thr Thr Pro Ile
 1 5 10 15
 Tyr Tyr Val Asn Asp Ile Pro His Ile Gly His Ala Tyr Thr Thr Leu
 20 25 30
 Ile Ala Asp Thr Leu Lys Lys Tyr Tyr Thr Leu Gln Gly Glu Glu Val
 35 40 45
 Phe Phe Leu Thr Gly Thr Asp Glu His Gly Gln Lys Ile Glu Gln Ser
 50 55 60
 Ala Arg Leu Arg Asn Gln Ser Pro Lys Ala Tyr Ala Asp Ser Ile Ser
 65 70 75 80
 Ala Ile Phe Lys Asn Gln Trp Asp Phe Phe Asn Leu Asp Tyr Asp Gly
 85 90 95
 Phe Ile Arg Thr Thr Asp Ser Glu His Gln Lys Cys Val Gln Asn Ala
 100 105 110
 Phe Glu Ile Met Phe Glu Lys Gly Asp Ile Tyr Lys Gly Thr Tyr Ser
 115 120 125
 Gly Tyr Tyr Cys Val Ser Cys Glu Ser Tyr Cys Ala Val Ser Lys Val
 130 135 140
 Asp Asn Thr Asp Ser Lys Val Leu Cys Pro Asp Cys Leu Arg Glu Thr
 145 150 155 160
 Thr Leu Leu Glu Glu Glu Ser Tyr Phe Phe Lys Leu Ser Ala Tyr Glu
 165 170 175
 Lys Pro Leu Leu Glu Phe Tyr Ala Lys Asn Pro Glu Ala Ile Leu Pro
 180 185 190
 Ile Tyr Arg Lys Asn Glu Val Thr Ser Phe Ile Glu Gln Gly Leu Leu
 195 200 205
 Asp Leu Ser Ile Thr Arg Thr Ser Phe Glu Trp Gly Ile Pro Leu Pro
 210 215 220
 Lys Lys Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala
 225 230 235 240
 Leu Leu Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn
 245 250 255
 Lys Met Ala His Phe Glu Arg Ala Arg His Ile Val Gly Lys Asp Ile
 260 265 270
 Leu Arg Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn

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275	280	285
Leu Pro Leu Phe Lys Gln Leu Cys Val His Gly Trp Trp Thr Ile Glu		
290	295	300
Gly Val Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys		
305	310	315
Leu Ala Met Glu Tyr Gly Ile Glu Glu Leu Arg Tyr Phe Leu Leu Arg		
	325	330
Glu Val Pro Phe Gly Gln Asp Gly Asp Phe Ser Lys Lys Ala Leu Val		
	340	345
Glu Arg Ile Asn Ala Asn Leu Asn Asn Asp Leu Gly Asn Leu Leu Asn		
	355	360
Arg Leu Leu Gly Met Ala Lys Lys Tyr Phe Asn Tyr Ser Leu Lys Ser		
	370	375
Thr Lys Ile Thr Ala Tyr Tyr Pro Lys Glu Leu Lys Ala His Gln		
385	390	395
Ile Leu Asp Asn Ala Asn Ser Phe Val Pro Lys Met Gln Leu His Lys		
	405	410
Ala Leu Glu Glu Leu Phe Asn Ile Tyr Asp Phe Leu Asn Lys Leu Ile		
	420	425
Ala Lys Glu Glu Pro Trp Val Leu His Lys Asn Asn Glu Ser Glu Lys		
	435	440
Leu Glu Ala Leu Leu Ser Leu Ile Ala Asn Thr Leu Leu Gln Ser Ser		
	450	455
Phe Leu Leu Tyr Ala Phe Met Pro Lys Ser Ala Met Lys Leu Ala Ser		
465	470	475
Ala Phe Arg Val Glu Ile Thr Pro Asn Asn Tyr Glu Arg Phe Phe Lys		
	485	490
Ala Lys Lys Leu Gln Asp Met Val Leu Gln Asp Thr Glu Pro Leu Phe		
	500	505
Ser Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu Lys Ile Glu		
	515	520
Lys Ile Glu Lys Gly Glu Glu Ala Leu Ala Glu Lys Ala Glu Lys Lys		
	530	535
Glu Lys Glu Lys Ala Pro Thr Gln Glu Asn Tyr Ile Ser Ile Glu		
545	550	555
Asp Phe Lys Lys Val Glu Ile Lys Val Gly Leu Ile Lys Glu Ala Gln		
	565	570
Arg Ile Glu Lys Ser Asn Lys Leu Leu Arg Leu Lys Val Asp Leu Gly		
	580	585
Glu Asn Arg Leu Arg Gln Ile Ile Ser Gly Ile Ala Leu Asp Tyr Glu		
	595	600
Pro Glu Ser Leu Val Gly Gln Met Val Cys Val Val Ala Asn Leu Lys		
	610	615
Pro Ala Lys Leu Met Gly Glu Met Ser Glu Gly Met Ile Leu Ala Val		
625	630	635
Arg Asp Asn Asp Asn Leu Ala Leu Ile Ser Pro Thr Arg Glu Lys Ile		
	645	650
Ala Gly Ser Leu Ile Ser		
	660	

(2) INFORMATION FOR SEQ ID NO:1864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1864

```

Gly Arg Met Met Lys Ile Val Ile Asp Leu Met Gly Ala Asp His Gly
1          5          10          15
Val Leu Pro Ile Ile Glu Gly Val Ser Arg Ala Leu Glu Asn Lys Ser
20          25          30
Phe Ser Val Val Leu Val Gly Asp Lys Asp Lys Ala Thr Pro Phe Ile
35          40          45
Ser Lys Glu Leu Ala Ser Lys Val Glu Met Ile His Thr Gln Asp Tyr
50          55          60
Ile Lys Met Glu Glu Ala Ala Thr Glu Ala Ile Lys Arg Lys Glu Ser
65          70          75          80
Ser Ile Tyr Leu Gly Met Asp Ile Leu Lys Asn Gly Ala Asp Ala Leu
85          90          95
Ile Ser Ala Gly His Ser Gly Ala Thr Met Gly Leu Ala Thr Leu Arg
100         105         110
Leu Gly Arg Ile Lys Gly Val Glu Arg Pro Ala Ile Cys Thr Leu Met
115         120         125
Pro Ser Val Gly Lys Arg Pro Ser Val Leu Leu Asp Ala Gly Ala Asn
130         135         140
Thr Asp Cys Lys Pro Glu Tyr Leu Ile Asp Phe Ala Leu Met Gly Tyr
145         150         155         160
Glu Tyr Ala Lys Ser Val Leu His Tyr Asp Ser Pro Lys Val Gly Leu
165         170         175
Leu Ser Asn Gly Glu Glu Asp Ile Lys Gly Asn Thr Leu Val Lys Glu
180         185         190
Thr His Lys Met Leu Lys Ala Tyr Asp Phe Phe Tyr Gly Asn Val Glu
195         200         205
Gly Ser Asp Ile Phe Lys Gly Val Val Asp Val Val Val Cys Asp Gly
210         215         220
Phe Met Gly Asn Val Val Leu Lys Thr Thr Glu Gly Val Ala Ser Ala
225         230         235         240
Ile Gly Ser Ile Phe Lys Asp Glu Ile Lys Ser Ser Phe Lys Ser Lys
245         250         255
Met Gly Ala Leu Met Leu Lys Asn Ala Phe Gly Ile Leu Lys Gln Lys
260         265         270
Thr Asp Tyr Ala Glu Tyr Gly Gly Ala Pro Leu Leu Gly Val Asn Lys
275         280         285
Ser Val Ile Ile Ser His Gly Lys Ser Asn Ala Arg Ala Val Glu Cys
290         295         300
Ala Ile Tyr Gln Ala Ile Ser Ala Val Glu Ser Gln Val Cys Leu Arg
305         310         315         320
Ile Thr Gln Ala Phe Glu Ser Leu Lys Ser Gln Ser Phe Glu Ser Gln
325         330         335
Ser Asp Gln Gln Asp Ala
340

```

(2) INFORMATION FOR SEQ ID NO:1865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

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(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1865

```

Asn Ala His Ala Phe Thr His Pro Phe Ser Ala Pro Ala Arg Phe Arg
1      5      10      15
Leu Ala Gln Lys Arg Lys Asp Asn Thr Leu Pro Phe Leu Arg Pro Asp
      20      25      30
Gly Lys Ser Gln Val Ser Val Arg Tyr Glu Asn Asn Lys Pro Val Ser
      35      40      45
Val Asp Thr Ile Val Ile Ser Thr Gln His Ser Pro Glu Val Ser Gln
      50      55      60
Lys His Leu Lys Glu Ala Val Ile Glu Glu Ile Val Tyr Lys Val Leu
65      70      75      80
Pro Lys Glu Tyr Leu His Asp Asn Ile Lys Phe Phe Ile Asn Pro Thr
      85      90      95
Gly Lys Phe Val Ile Gly Gly Pro Gln Gly Asp Ala Gly Leu Thr Gly
      100      105      110
Arg Lys Ile Ile Trp Asp Thr Tyr Gly Gly Phe Cys Pro His Gly Gly
      115      120      125
Gly Ala Phe Thr Gly Lys Asp Pro Tyr Lys Val Asp Met Ser Ala Ala
      130      135      140
Tyr Ala Ala Arg Tyr Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys
145      150      155      160
Asp Lys Ala Thr Val Gln Leu Ala Tyr Ala Ile Gly Val Ile Glu Pro
      165      170      175
Val Ser Ile Tyr Val Asn Thr His Asn Thr Ser Lys His Ser Ser Ala
      180      185      190
Glu Leu Glu Lys Cys Val Lys Ser Val Phe Lys Leu Thr Pro Lys Gly
      195      200      205
Ile Ile Glu Ser Leu Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser
      210      215      220
Ala Tyr Gly His Phe Gly Arg Glu Leu Glu Glu Phe Thr Trp Glu Lys
225      230      235      240
Thr Asn Lys Val Glu Glu Ile Lys Ala Phe Phe Lys Arg
      245      250

```

(2) INFORMATION FOR SEQ ID NO:1866:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION 1...145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1866

```

Ser Thr Ile His Lys Glu Phe Lys Leu Lys Gln Arg Thr Leu Ser Ile
1      5      10      15
Ile Lys Pro Asp Ala Leu Lys Lys Lys Val Val Gly Lys Thr Ile Asp
      20      25      30

```

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```

Arg Phe Glu Ser Asn Gly Leu Glu Val Val Ala Met Lys Arg Leu His
   35           40           45
Leu Ser Val Lys Asp Ala Glu Asn Phe Tyr Ala Ile Leu Arg Glu Arg
   50           55           60
Pro Phe Phe Lys Asp Leu Ile Glu Phe Met Val Ser Gly Pro Val Val
   65           70           75           80
Val Met Val Leu Glu Gly Lys Asp Ala Val Ala Lys Asn Arg Glu Leu
           85           90           95
Met Gly Ala Thr Asp Pro Lys Leu Ala Gln Lys Gly Thr Ile Arg Ala
           100          105          110
Asp Phe Ala Glu Ser Ile Asp Ala Asn Ala Val His Gly Ser Asp Ser
           115          120          125
Leu Glu Asn Ala His Asn Glu Ile Ala Phe Phe Phe Ala Ala Arg Glu
   130           135           140
Phe
145

```

(2) INFORMATION FOR SEQ ID NO:1867:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1867

```

Gly Arg Gly Gly Ile Tyr Ile Glu His Gly Arg Val Lys Met Val Ala
1      5      10      15
Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala Gly Tyr Lys
   20      25      30
Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr Val Lys Ile
   35      40      45
Phe Lys Ile Asp Leu Ser Glu Phe Glu Pro Leu Glu Asn Tyr Lys Ser
   50      55      60
Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Lys Glu Arg Pro Phe Asp
   65      70      75      80
Lys Ala Pro Asn Ile Cys Ile Ala Pro Cys Asp Ala Leu Ile Thr Glu
           85      90      95
Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys Gly Met Pro
           100     105     110
Tyr Lys Ala His Glu Leu Val Gly Glu Ile Asn Pro Leu Ser Pro Ser
           115     120     125
Phe Phe Tyr Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr
           130     135     140
His Ala Pro Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly
145      150      155      160
Lys Leu Leu Pro Val Asn Lys Pro Ser Leu His Lys Asn Lys Asn Leu
           165     170     175
Phe Val Gly Asn Glu Arg Val Ala Leu Val Ala Lys Asp Asp Ser Arg
           180     185     190
Gln

```

1394

(2) INFORMATION FOR SEQ ID NO:1868:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1868

```

Asn His Asn Lys Gly Ala Glu Ile Ser Leu Trp Gly Leu Thr Arg Leu
1      5      10      15
Val Asp Arg Asp Ile Asp Lys Asp Asn Pro Arg Thr Lys Asn Arg Pro
20     25     30
Ser Val Asp Gly Arg Ile Ser Val Lys Gly Met Val Ile Phe Ser Val
35     40     45
Ser Asn Ala Ile Leu Phe Val Gly Trp Ser Asn Phe Ile Asn Pro Leu
50     55     60
Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile Ile Leu Gly Gly Tyr Ser
65     70     75     80
Tyr Phe Lys Arg Phe Ser Ser Leu Ala His Phe Val Val Gly Leu Ala
85     90     95
Leu Gly Leu Ala Pro Ile Ala Gly Ser Val Ala Val Leu Gly Asp Ile
100    105    110
Pro Leu Trp Asn Val Phe Leu Ala Leu Gly Val Met Leu Trp Val Ala
115    120    125
Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp Met Glu Phe Asp Lys Glu
130    135    140
Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu Gly Glu Lys Trp Cys Leu
145    150    155    160
Asn Leu Ser Arg Leu Ser His Leu Val Ala Leu Ile Cys Trp Leu Cys
165    170    175
Phe Val Lys Cys Tyr His Gly Gly Leu Phe Ala Tyr Leu Gly Leu Gly
180    185    190
Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln Ile Leu Val Ala Arg Asp
195    200    205
Tyr Lys Asn Ile Pro Lys Ala Phe Phe Val Ser Asn Gly Tyr Leu Gly
210    215    220
Val Val Phe Phe Ile Phe Ile Val Leu Asp Val Gly Phe Lys His Ala
225    230    235    240

```

(2) INFORMATION FOR SEQ ID NO:1869:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

SUBSTITUTE SHEET (RULE 26)

1395

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1869

```

Val Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Leu Ser Ser Leu Met
1           5           10           15
Trp Gly Ser Ser Met His Glu Leu Val Leu Arg Ser Gln Ala Leu Gly
           20           25           30
Phe Glu Thr Arg Leu Val Gln Cys Asp Leu Ser Phe Ser Tyr Glu Arg
           35           40           45
Phe Ile Ser Lys Thr Lys Arg Ser Leu Ala Val Leu Glu Glu Phe Asp
           50           55           60
Trp Leu Asn Ser Gly Phe Asp Phe Ser Arg Leu Asn Val Glu Asn Asp
65           70           75           80
Thr Leu Glu Leu Leu Lys Ala Leu Tyr Phe Lys Leu Glu Lys Leu Glu
           85           90           95
Ser Leu Leu Leu Lys Glu Asn Leu Leu Glu Leu Glu Gln Lys Asp Arg
           100          105          110
Ile Ile Ala Leu Gly His Gly Leu Val Cys Leu Lys Lys Gln Ser Leu
           115          120          125
Ile Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Glu Gly Lys Ile
           130          135          140
Leu Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Glu Ile Thr
145          150          155          160
Arg Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp
           165          170          175
Ser Glu Arg Lys Gly Leu Lys Leu
           180

```

(2) INFORMATION FOR SEQ ID NO:1870:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1870

```

Thr Gly Ala Ile Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu
1           5           10           15
Gly Ala Ile Leu Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu
           20           25           30
Lys Glu Lys Glu Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu
           35           40           45
Asp Glu Ser Tyr Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu
           50           55           60
Leu Glu Gly Arg Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu
65           70           75           80
Asp Ser Ser Leu Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln

```

SUBSTITUTE SHEET (RULE 26)

1396

85 90 95
 Glu Ile Gln Lys Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys
 100 105 110
 Ile Ile Thr
 115

(2) INFORMATION FOR SEQ ID NO:1871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...335

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1871

Glu Pro Ile Lys Ser Asp Lys Glu Ala Phe Asp Leu Val Met Gln Asn
 1 5 10 15
 Arg Ser His Glu Ile Gln Gly Val Ser His Ile Lys Asn Asn Tyr Lys
 20 25 30
 Phe Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly Tyr Arg Ile
 35 40 45
 Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val Ala Ile Gly
 50 55 60
 Leu Glu Leu Gly Glu Asp Asp Pro Gln Val Val Phe Glu Ser Ile Asn
 65 70 75 80
 Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg Asn Tyr Leu
 85 90 95
 Met Met Gly Glu Asn Ser Asp Asn Gln Asn Arg Leu Tyr Asn Thr Tyr
 100 105 110
 Trp Val Pro Leu Glu Asn Trp Leu Gly Glu Lys Asp Leu Asn Asp Phe
 115 120 125
 Ile Lys Thr Tyr Leu Arg Ile Tyr Phe Glu Asp Arg Val Lys Glu Gly
 130 135 140
 Glu Arg Glu Val Tyr Tyr Ala Leu Lys Ala His His Arg Asp Asn Phe
 145 150 155 160
 Pro Asn Asn Ile Gln Gly Leu Met Ser Asp Met Arg Glu Tyr Gly Arg
 165 170 175
 Ile Phe Gln Ile Phe Leu Asp Arg Asp His Tyr Phe Leu His Arg Gly
 180 185 190
 Asp Pro Gln Gln Leu Ala Asn Leu Arg Leu Arg Val Lys Asp Leu Val
 195 200 205
 Lys Ile Lys Phe Gly Val Ala Lys Pro Phe Val Leu Arg Cys Ala Arg
 210 215 220
 Asp Phe Glu Glu Gly Lys Leu Asp Tyr Glu Asn Phe His Glu Ile Leu
 225 230 235 240
 Gln Ile Leu Ile Ser Tyr Phe Val Arg Arg Ser Val Cys Gly Asp Ser
 245 250 255
 Thr Pro Thr Leu Thr Arg Val Leu Tyr Ser Leu Tyr Arg Gln Leu Gly
 260 265 270
 Glu Asp Val Ser Ala Asp Ala Leu Lys Arg Tyr Leu Gly Lys Ser Val
 275 280 285
 Gly Gln Met Ala Phe Pro Asn Asp Asp Lys Ile Lys Ala Ala Phe Leu
 290 295 300

1397

```

Val Arg Asn Ala Tyr Ala Ala Asn Gln Val Cys Lys Phe Ile Leu Leu
305          310          315          320
Glu Ile Glu Lys Leu Ala Thr Leu Asn Arg Gln Lys Lys Arg Ile
          325          330          335

```

(2) INFORMATION FOR SEQ ID NO:1872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1872

```

Phe Tyr Val Ser Ile Ile Lys Cys Thr Pro Leu Leu Val Gln Ile Val
1          5          10          15
Ile Val Phe Tyr Gly Leu Pro Ala Leu Gly Val Tyr Met Asp Pro Ile
          20          25          30
Pro Ala Gly Ile Ile Ala Phe Ser Phe Asn Val Gly Ala Tyr Ala Ser
          35          40          45
Glu Thr Leu Arg Ala Ser Phe Leu Ser Val Pro Lys Asp Gln Trp Asp
          50          55          60
Ser Ser Leu Ser Leu Gly Leu Asn Tyr Leu Gln Thr Phe Trp His Val
65          70          75          80
Ile Phe Phe Gln Ala Leu Lys Val Ala Thr Ala Lys Pro Lys
          85          90

```

(2) INFORMATION FOR SEQ ID NO:1873:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...461

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1873

```

Ser Ile Lys His Leu Gly Lys Lys Glu Val Lys Thr Leu Gly Leu Ser
1          5          10          15
Ser Leu Gly Gly Thr Leu Glu Phe Tyr Asp Phe Ile Ile Phe Val Phe
          20          25          30
Phe Thr Ser Ile Ile Ala Lys His Phe Phe Pro Asn Thr Leu Ser Pro

```

SUBSTITUTE SHEET (RULE 26)

1398

```

      35      40      45
Ile Trp Ser Glu Ile Asn Thr Tyr Gly Ile Phe Ala Ala Gly Tyr Leu
50      55      60
Ala Arg Pro Leu Gly Gly Ile Val Met Ala His Phe Gly Asp Lys Phe
65      70      75      80
Gly Arg Lys Asn Met Phe Met Leu Ser Ile Leu Leu Met Val Ile Pro
      85      90      95
Thr Phe Ala Leu Ala Leu Met Pro Thr Phe Asn Asp Leu Val Gly Phe
      100      105      110
Gly Val Asp Ser Met Gly Leu Thr Pro Lys Asn Ala His Tyr Leu Gly
      115      120      125
Tyr Ile Ala Pro Val Phe Leu Val Leu Val Arg Ile Cys Gln Gly Val
      130      135      140
Ala Val Gly Gly Glu Leu Pro Gly Ala Trp Val Phe Val His Glu His
      145      150      155      160
Ala Pro Gln Gly Gln Lys Asn Thr Tyr Ile Gly Phe Leu Thr Ala Ser
      165      170      175
Val Val Ser Gly Ile Leu Leu Gly Ser Leu Val Tyr Ile Gly Ile Tyr
      180      185      190
Met Val Phe Asp Lys Pro Val Val Glu Asp Trp Ala Trp Arg Val Ala
      195      200      205
Phe Gly Leu Gly Gly Ile Phe Gly Ile Ile Ser Val Tyr Leu Arg Arg
      210      215      220
Phe Leu Glu Glu Thr Pro Val Phe Gln Gln Met Lys Gln Asp Asp Ala
      225      230      235      240
Leu Val Lys Phe Pro Leu Lys Glu Val Phe Lys Asn Ser Leu Phe Gly
      245      250      255
Ile Ser Ile Ser Met Leu Ile Thr Trp Val Leu Thr Ala Cys Ile Leu
      260      265      270
Ile Phe Ile Leu Phe Val Pro Asn Phe Thr Leu Thr His Pro Asn Phe
      275      280      285
His Phe Thr Pro Phe Glu Lys Thr Tyr Phe Gln Ile Leu Gly Leu Val
      290      295      300
Gly Ile Val Ser Ser Ile Ile Phe Thr Gly Phe Leu Ala Asp Lys Ile
      305      310      315      320
Lys Pro His Lys Val Cys Met Ala Phe Ser Ala Ala Phe Gly Phe Phe
      325      330      335
Gly Phe Leu Phe Phe Lys Glu Phe Tyr Ser Asn Ala Pro Ser Leu Val
      340      345      350
Asn Thr Ile Ile Leu Tyr Phe Leu Ala Cys Phe Cys Ala Gly Ile Met
      355      360      365
Asn Phe Cys Pro Ile Phe Met Ser Asp Val Phe Ser Ala Arg Ile Arg
      370      375      380
Phe Ser Gly Ile Ser Phe Ala Tyr Asn Ile Ala Tyr Ala Ile Thr Ala
      385      390      395      400
Gly Phe Thr Pro Gln Leu Ser Ser Trp Leu Asn Ala Lys Ala Ile Ala
      405      410      415
Val Pro Glu Ser Leu Gln Ser Tyr Gly Leu Ser Phe Tyr Ile Leu Ile
      420      425      430
Val Ser Leu Ile Ala Phe Ile Thr Ser Leu Leu Met Ala Pro Ile Tyr
      435      440      445
His Lys Ser Asn Thr Gln His Glu Val Ser Pro Thr Ala
      450      455      460

```

(2) INFORMATION FOR SEQ ID NO:1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

SUBSTITUTE SHEET (RULE 26)

1399

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1874

```

Lys Ser Leu Lys Lys Lys Cys Arg Ser Phe Leu Gln Glu Tyr Glu Val
1      5      10      15
Tyr Ser Leu Asp Leu Ala Leu Met Val Ala Gly Ala Lys Tyr Arg Gly
20      25      30
Asp Phe Glu Lys Arg Leu Lys Lys Thr Leu Lys Glu Ile Gln Gln Asn
35      40      45
Gly Arg Ile Ile Leu Phe Ile Asp Glu Ile His Thr Leu Leu Gly Ala
50      55      60
Gly Ser Ser Asn Ala Gly Ser Leu Asp Ala Ala Asn Ile Leu Lys Pro
65      70      75      80
Val Leu Thr Asp Gly Ser Leu Lys Cys Leu Gly Ala Thr Thr Phe Glu
85      90      95
Glu Tyr Arg Ser Val Phe Glu Lys Asp Lys Ala Phe Asn Arg Arg Phe
100      105      110
Ser Ile Val Asn Val Glu Glu Pro Ser Lys Glu Ala Cys Tyr Leu Ile
115      120      125
Leu Lys Asn Ile Ala Pro Leu Tyr Glu Glu His His Gln Val Arg Tyr
130      135      140
Asn Glu Ser Val Phe Lys Ala Cys Val Asp Leu Thr Ser Tyr Tyr Met
145      150      155      160
His Asp Lys Phe Leu Pro Asp Lys Ala Ile Glu Leu Leu Asp Glu Val
165      170      175
Gly Ser Arg Lys Lys Ile Asn Pro Lys Lys Gly Lys Lys Ile Ser Val
180      185      190
Asp Asp Val Gln Glu Thr Leu Ala Leu Lys Leu Lys Ile Pro Lys Met
195      200      205
Arg Leu Asn Ser Asp Lys Lys Ala Leu Leu Arg Asn Leu Glu Lys Ser
210      215      220
Leu Lys Asn Lys Ile Phe Ala Gln Thr Glu Ala Ile Asn Leu Val Ser
225      230      235      240
Asn Ala Ile Lys Ile Gln His Cys Gly Leu Ser Ala Lys Asn Lys Pro
245      250      255
Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
260      265      270
Leu Ala Lys Glu Leu Ala Leu Asn Leu Asn Leu His Phe Glu Arg Phe
275      280      285
Asp Met Ser Glu Tyr Lys Glu Ala His Ser Val Ala Lys Leu Ile Gly
290      295      300
Ser Pro Ser Gly Tyr Val Gly Phe Glu Gln Gly Gly Leu Leu Val Asn
305      310      315      320
Ala Ile Lys Lys His Pro His Cys Leu Leu Leu Leu Asp Glu Ile Glu
325      330      335
Lys Ala His Pro Asn Val Tyr Asp Leu Leu Leu Gln Val Met Asp Asn
340      345      350
Ala Thr Leu Ser Asp Asn Leu Gly Asn Lys Ala Ser Phe Lys His Val
355      360      365
Ile Leu Ile Met Thr Ser Asn Val Gly Ser Lys Asp Lys Asp Thr Leu
370      375      380
Gly Phe Phe Ser Thr Lys Asn Ala Lys Tyr Asp Arg Ala Val Lys Glu
385      390      395      400
Leu Leu Thr Pro Glu Leu Arg Ser Arg Ile Asp Ala Ile Val Pro Phe
405      410      415
Asn Ala Leu Ser Leu Glu Asp Phe Glu Arg Ile Val Ser Val Glu Leu
420      425      430
Asp Gly Leu Lys Ala Leu Ala Ile Glu Gln Gly Val Ile Leu Lys Phe

```

SUBSTITUTE SHEET (RULE 26)

1400

```

      435              440              445
His Lys Glu Val Val Lys Cys Ile Ala Gln Lys Ser Tyr Gln Arg Ser
  450              455              460
Phe Gly Ala Arg Glu Ile Lys Lys Ile Ile Gln Arg Glu Ile Asn Pro
  465              470              475              480
Gln Leu Ser Asp Ile Val Leu Lys Gln Ser Leu Lys Lys Pro Thr Arg
      485              490              495
Ser Leu Arg Met Lys Ser Thr Phe His Lys Val
      500              505

```

(2) INFORMATION FOR SEQ ID NO:1875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1875

```

Gly Ile Lys Leu Ile Lys Phe Val Arg Asn Val Val Leu Phe Ile Leu
 1              5              10              15
Thr Ala Ile Phe Leu Ala Phe Met Leu Val Ser Tyr Cys Met Pro
      20              25              30
His Tyr Ser Val Ala Val Ile Ser Gly Val Glu Val Lys Arg Met Asn
      35              40              45
Glu Asn Glu Asn Thr Pro Asn Asn Lys Glu Val Lys Thr Leu Ala Arg
      50              55              60
Asp Val Tyr Phe Val Gln Thr Tyr Asp Pro Lys Asp Gln Lys Ser Val
      65              70              75              80
Thr Val Tyr Arg Asn Glu Asp Thr Arg Phe Gly Phe Pro Phe Tyr Phe
      85              90              95
Lys Phe Asn Ser Ala Asp Ile Ser Ala Leu Ala Gln Ser Leu Val Asn
      100              105              110
Gln Gln Val Glu Val Gln Tyr Tyr Gly Trp Arg Ile Asn Leu Phe Asn
      115              120              125
Met Phe Pro Asn Val Ile Phe Leu Lys Pro Leu Lys Glu Ser Asp Glu
      130              135              140
Met Ser Lys Pro Val Phe Ser Trp Ile Leu Tyr Ala Leu Leu Leu Val
      145              150              155              160
Gly Phe Phe Ile Ser Ala Arg Ser Val Cys Thr Leu Phe Lys Gly Lys
      165              170              175
Ala His

```

(2) INFORMATION FOR SEQ ID NO:1876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

1401

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...638

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1876

```

Ala Arg Leu Leu Leu Tyr Asn Leu Lys Asn Phe Ile Lys Gly Lys Ser
1      5      10      15
Ser Met Ser Asn Gln Glu Tyr Thr Phe Gln Thr Glu Ile Asn Gln Leu
20      25      30
Leu Asp Leu Met Ile His Ser Leu Tyr Ser Asn Lys Glu Ile Phe Leu
35      40      45
Arg Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Asp Lys Leu Asn Tyr
50      55      60
Leu Met Leu Thr Asp Glu Lys Leu Lys Gly Leu Asn Thr Thr Pro Ser
65      70      75      80
Ile His Leu Ser Phe Asp Ser Gln Lys Lys Thr Leu Thr Ile Lys Asp
85      90      95
Asn Gly Ile Gly Met Asp Lys Ser Asp Leu Ile Glu His Leu Gly Thr
100     105     110
Ile Ala Lys Ser Gly Thr Lys Ser Phe Leu Ser Ala Leu Ser Gly Asp
115     120     125
Lys Lys Lys Asp Ser Ala Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr
130     135     140
Ser Ala Phe Met Val Ala Ser Lys Ile Val Val Gln Thr Lys Lys Val
145     150     155     160
Thr Ser His Gln Ala Tyr Ala Trp Val Ser Asp Gly Lys Gly Lys Phe
165     170     175
Glu Ile Ser Glu Cys Val Lys Glu Glu Gln Gly Thr Glu Ile Thr Leu
180     185     190
Phe Leu Lys Glu Glu Asp Ser His Phe Ala Ser Arg Trp Glu Ile Asp
195     200     205
Ser Val Val Lys Lys Tyr Ser Glu His Ile Pro Phe Pro Ile Phe Leu
210     215     220
Thr Tyr Thr Asp Thr Lys Phe Glu Gly Glu Gly Asp Asn Lys Lys Glu
225     230     235     240
Val Lys Glu Glu Lys Cys Asp Gln Ile Asn Gln Ala Ser Ala Leu Trp
245     250     255
Lys Met Asn Lys Ser Glu Leu Lys Glu Lys Asp Tyr Lys Asp Phe Tyr
260     265     270
Gln Ser Phe Ala His Asp Asn Ser Glu Pro Leu Ser Tyr Ile His Asn
275     280     285
Lys Val Glu Gly Ser Leu Glu Tyr Thr Thr Leu Phe Tyr Ile Pro Ser
290     295     300
Lys Ala Pro Phe Asp Leu Phe Arg Val Asp Tyr Lys Ser Gly Val Lys
305     310     315     320
Leu Tyr Val Lys Arg Val Phe Ile Thr Asp Asp Asp Lys Glu Leu Leu
325     330     335
Pro Ser Tyr Leu Arg Phe Val Lys Gly Val Ile Asp Ser Glu Asp Leu
340     345     350
Pro Leu Asn Val Ser Arg Glu Ile Leu Gln Gln Asn Lys Ile Leu Ala
355     360     365
Asn Ile Arg Ser Ala Ser Val Lys Lys Ile Leu Ser Glu Ile Glu Arg
370     375     380
Leu Ser Lys Asp Asn Lys Asn Tyr His Lys Phe Tyr Glu Pro Phe Gly
385     390     395     400
Lys Val Leu Lys Glu Gly Leu Tyr Gly Asp Phe Glu Asn Lys Glu Lys
405     410     415
Leu Leu Glu Leu Leu Arg Phe Tyr Ser Lys Asp Lys Gly Glu Trp Ile

```

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1402

```

          420          425          430
Ser Leu Lys Glu Tyr Lys Glu Asn Leu Lys Glu Asn Gln Lys Ser Ile
          435          440          445
Tyr Tyr Leu Leu Gly Glu Asn Leu Asp Leu Leu Lys Ala Ser Pro Leu
          450          455          460
Leu Glu Lys Tyr Ala Gln Lys Gly Tyr Asp Val Leu Leu Leu Ser Asp
          465          470          475          480
Glu Ile Asp Ala Phe Val Met Pro Gly Val Asn Glu Tyr Asp Lys Thr
          485          490          495
Pro Phe Arg Asp Ala Ser His Ser Glu Ser Leu Lys Glu Leu Gly Leu
          500          505          510
Ala Glu Ile His Asp Glu Val Lys Asp Gln Phe Lys Asp Leu Ile Lys
          515          520          525
Ala Phe Glu Glu Asn Leu Lys Asp Glu Ile Lys Gly Val Glu Leu Ser
          530          535          540
Gly His Leu Thr Ser Ala Val Ala Leu Ile Gly Asp Glu Pro Asn Ala
          545          550          555          560
Met Met Ala Asn Trp Met Arg Gln Met Gly Gln Ser Val Pro Glu Ser
          565          570          575
Lys Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu
          580          585          590
Leu Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu
          595          600          605
Tyr Asp Gly Ala Lys Leu Leu Glu Lys Gly Ala Leu Lys Asp Ala Lys
          610          615          620
Ser Phe Asn Glu Arg Leu Asn Ser Val Leu Leu Lys Ala Leu
          625          630          635

```

(2) INFORMATION FOR SEQ ID NO:1877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1877

```

Lys Gln Phe Gly Arg Arg Val Phe Thr Gln Ile Pro Lys Met Val Gln
1          5          10          15
Phe Gln Asn Thr Leu Ile Lys Phe His Ala Leu Ser Phe Lys Asn Ala
          20          25          30
Asn Leu Ile Tyr Asn Ala Lys Leu Asn Lys Thr Cys Tyr Lys Glu Asn
          35          40          45
Ser Asn Thr Ile Ile Leu Arg Ile Lys Met Leu Thr Gln Glu Asp Val
          50          55          60
Leu Asn Ala Leu Lys Thr Ile Ile Tyr Pro Asn Phe Glu Lys Asp Ile
          65          70          75          80
Val Ser Phe Gly Phe Val Lys Asn Ile Thr Leu His Asp Asn Gln Leu
          85          90          95
Gly Leu Leu Ile Glu Ile Pro Ser Ser Glu Glu Thr Ser Ala Ile
          100          105          110
Leu Arg Glu Asn Ile Ser Lys Ala Met Gln Glu Lys Gly Val Lys Ala
          115          120          125

```


1403

```

Leu Asn Leu Asp Ile Lys Thr Pro Pro Lys Pro Gln Ala Pro Lys Pro
130      135      140
Thr Thr Lys Asn Leu Ala Lys Asn Ile Lys His Val Val Met Ile Ser
145      150      155      160
Ser Gly Lys Gly Gly Val Gly Lys Ser Thr Thr Ser Val Asn Leu Ser
      165      170      175
Ile Ala Leu Ala Asn Leu Asn Gln Lys Val Gly Leu Leu Asp Ala Asp
      180      185      190
Val Tyr Gly Pro Asn Ile Pro Arg Met Met Gly Leu Gln Asn Ala Asp
195      200      205
Val Ile Met Asp Pro Ser Gly Lys Lys Leu Ile Pro Leu Lys Ala Phe
210      215      220
Gly Val Ser Val Met Ser Met Gly Leu Leu Tyr Asp Glu Gly Gln Ser
225      230      235      240
Leu Ile Trp Arg Gly Pro Met Leu Met Arg Ala Ile Glu Gln Met Leu
      245      250      255
Ser Asp Ile Ile Trp Gly Asp Leu Asp Val Leu Val Val Asp Met Pro
      260      265      270
Pro Gly Thr Gly Asp Ala Gln Leu Thr Leu Ala Gln Ala Val Pro Leu
275      280      285
Ser Ala Gly Ile Thr Val Thr Thr Pro Gln Ile Val Ser Leu Asp Asp
290      295      300
Ala Lys Arg Ser Leu Asp Met Phe Lys Lys Leu His Ile Pro Ile Ala
305      310      315      320
Gly Ile Val Glu Asn Met Gly Ser Phe Val Cys Glu His Cys Lys Lys
      325      330      335
Glu Ser Glu Ile Phe Gly Ser Asn Ser Met Ser Gly Leu Leu Glu Ala
      340      345      350
Tyr Asn Thr Gln Ile Leu Ala Lys Leu Pro Leu Glu Pro Lys Val Arg
355      360      365
Leu Gly Gly Asp Lys Gly Glu Pro Ile Val Ile Ser His Pro Thr Ser
370      375      380
Val Ser Ala Lys Ile Phe Glu Lys Met Ala Lys Asp Leu Ser Ala Phe
385      390      395      400
Leu Asp Lys Val Glu Arg Glu Lys Leu Ala Asp Asn Lys Asp Ile Gln
      405      410      415
Pro Thr Gln Thr His Ala Tyr Ser His
      420      425

```

(2) INFORMATION FOR SEQ ID NO:1878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1878

```

Leu Gly Phe Leu Ala Leu His Gly Phe Phe Leu Ser Ala Phe Glu Tyr
1      5      10      15
Gln Val Ser Ala Arg Val Gly Ser Phe Ser Arg Ile Ala Phe Asn Gln
20     25     30
Ser Ile Ile Asn Ser Lys Lys Gly Ile Tyr Pro Thr Gly Ser Tyr Val

```

SUBSTITUTE SHEET (RULE 26)

1404

[illegible]

(2) INFORMATION FOR SEQ ID NO:1879:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

1405

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1879

```

Tyr Pro Thr Asn Thr Ile Ile Glu Arg Ile Leu Met Phe Lys Lys Met
1      5      10      15
Cys Leu Ser Leu Leu Met Ile Ser Gly Val Cys Val Gly Ala Lys Asp
      20      25      30
Leu Asp Phe Lys Leu Asp Tyr Arg Ala Thr Gly Gly Lys Phe Met Gly
      35      40      45
Lys Met Thr Asp Ser Ser Leu Leu Ser Ile Thr Ser Met Asn Asp Glu
      50      55      60
Pro Val Val Ile Lys Asn Leu Ile Val Asn Arg Gly Asn Ser Val Glu
      65      70      75      80
Ala Thr Lys Lys Val Glu Pro Lys Phe Gly Asp Lys Phe Lys Lys Glu
      85      90      95
Lys Leu Phe Asp His Glu Leu Lys Tyr Ser Gln Gln Ile Phe Tyr Arg
      100      105      110
Leu Asp Cys Lys Pro Asn Gln Leu Leu Glu Val Lys Ile Ile Thr Asp
      115      120      125
Lys Gly Glu Tyr Tyr His Lys Phe Ser Lys
      130      135

```

(2) INFORMATION FOR SEQ ID NO:1880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1880

```

Arg Ile Gly Met Asp Ala Leu Glu Ile Thr Gln Lys Leu Ile Ser Tyr
1      5      10      15
Pro Thr Ile Thr Pro Lys Glu Cys Gly Ile Phe Glu Tyr Ile Lys Ser
      20      25      30
Leu Phe Pro Ala Phe Lys Thr Leu Glu Cys Glu Lys Asn Gly Val Lys
      35      40      45
Asn Leu Phe Leu Tyr Arg Ile Phe Asn Pro Leu Lys Lys His Ala Glu
      50      55      60
Lys Glu His Ala Lys Glu Lys His Val Lys Glu Asn Val Lys Pro Leu
      65      70      75      80
His Phe Cys Phe Ala Gly His Ile Asp Val Val Pro Pro Gly Asn Asn
      85      90      95
Trp Gln Ser Asp Pro Phe Lys Pro Ile Ile Lys Glu Gly Phe Leu Tyr
      100      105      110
Gly Arg Gly Ala Gln Asp Met Lys Gly Gly Val Gly Ala Phe Leu Ser
      115      120      125
Ala Ser Leu Asn Phe Asn Pro Lys Thr Pro Phe Leu Leu Ser Ile Leu

```

1406

```

      130              135              140
Leu Thr Ser Asp Glu Glu Gly Pro Gly Ile Phe Gly Thr Arg Leu Met
145              150              155              160
Leu Glu Lys Leu Lys Glu Lys Asp Leu Leu Pro His Met Ala Ile Val
      165              170              175
Ala Glu Pro Thr Cys Glu Lys Val Leu Gly Asp Ser Ile Lys Ile Gly
      180              185              190
Arg Arg Gly Ser Ile Asn Gly Lys Leu Ile Leu Lys Gly Val Gln Gly
      195              200              205
His Val Ala Tyr Pro Gln Lys Cys Gln Asn Pro Ile Asp Thr Leu Ala
      210              215              220
Ser Val Leu Pro Leu Ile Ser Gly Val His Leu Asp Asn Gly Asp Glu
225              230              235              240
Cys Phe Asp Pro Ser Lys Leu Val Ile Thr Asn Leu His Ala Gly Leu
      245              250              255
Gly Ala Asn Asn Val Thr Pro Gly Ser Val Glu Ile Ala Phe Asn Ala
      260              265              270
Arg His Ser Leu Lys Thr Thr Gln Glu Ser Leu Lys Glu Tyr Leu Glu
      275              280              285
Lys Val Leu Lys Asp Leu Pro Tyr Thr Leu Glu Leu Glu Ser Ser Ser
290              295              300
Ser Pro Phe Ile Thr Ala Ser His Ser Lys Leu Thr Ser Val Leu Gln
305              310              315              320
Glu Asn Ile Leu Lys Thr Cys His Thr Thr Pro Leu Leu Asn Thr Lys
      325              330              335
Gly Gly Thr Ser Asp Ala Arg Phe Phe Ser Ala His Gly Ile Glu Val
      340              345              350
Val Glu Phe Gly Ala Ile Asn Asp Arg Ile His Ala Val Asp Glu Arg
      355              360              365
Val Ser Leu Lys Glu Leu Glu Leu Leu Glu Lys Val Phe Leu Gly Val
370              375              380
Leu Glu Gly Leu Ser Glu Lys
385              390

```

(2) INFORMATION FOR SEQ ID NO:1881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 928 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1881

```

Thr Ser Leu Asp His Lys Ile Thr Asp Phe Ser Cys Val Asp Leu Arg
1              5              10              15
Ile Gln Ser Lys Glu Val Ser His Asn Leu Lys Glu Leu Ser Lys Thr
      20              25              30
Leu Ile Ser Tyr Pro Phe Glu Lys His Val Glu Ala Leu Gly Glu Gln
      35              40              45
Cys Ser Asn Phe Val Ser Ile Pro Ile Asn Asn Asp Asp Tyr Ser Asn
50              55              60
Ile Cys Thr Phe Val Ser Asp Phe Ile Asn Leu Ile Ala Ser Tyr Asn
65              70              75              80

```

SUBSTITUTE SHEET (RULE 26)

1407

Leu Leu Glu Ser Phe Leu Asp Phe Tyr Lys Asp Lys Leu Lys Leu Ser
 85 90 95
 Glu Leu Val Thr Glu Tyr Ala Asn Val Thr Asn Asn Leu Leu Phe Lys
 100 105 110
 Lys Leu Ile Lys His Leu Ser Gly Asn Asn Gln Leu Val Lys Asn Phe
 115 120 125
 Tyr Gln Cys Ile Arg Glu Ile Ile Lys Tyr Asn Ala Pro Asn Lys Glu
 130 135 140
 Tyr Lys Pro Asn Gln Phe Phe Ile Ile Gly Lys Gly Lys Gln Lys Gln
 145 150 155 160
 Leu Ala Lys Ile Tyr Ser His Leu Lys Glu Leu Ser Ala Ser Glu Ile
 165 170 175
 Lys Pro Gln Asp Met Glu Asp Ile Leu Lys Lys Leu Glu Glu Leu Asp
 180 185 190
 Lys Ile Phe Lys Thr Thr Asp Phe Thr Lys Phe Thr Pro Lys Thr Glu
 195 200 205
 Ile Lys Asp Ile Ile Lys Glu Ile Asp Glu Lys Tyr Pro Ile Asn Glu
 210 215 220
 Asn Phe Lys Arg Gln Phe Asn Glu Phe Glu Ser Asn Ile Glu Lys His
 225 230 235 240
 Asp Glu Ile Lys Lys Asp Phe Glu Arg Asn Lys Glu Ser Leu Ile Arg
 245 250 255
 Glu Ile Glu Asn His Cys Lys Asn Glu Cys Asn Ser Glu Glu Glu Pro
 260 265 270
 Glu Tyr Lys Ile Asn Asp Leu Leu Lys Asn Ile Gln Gln Ile Cys Lys
 275 280 285
 Asn Tyr Ile Glu Ser His Ala Val Asn Asp Val Ser Lys Asp Ile Lys
 290 295 300
 Ser Met Met Cys Gln Phe Tyr Leu Lys Gln Ile Asp Leu Leu Val Asn
 305 310 315 320
 Ser Glu Ile Val Arg Tyr Arg Tyr Ser Asn Leu Phe Glu Pro Ile Gln
 325 330 335
 Arg Ser Leu Trp Glu Ser Ile Lys Ile Leu Asp Asn Glu Ser Gly Ile
 340 345 350
 Tyr Leu Phe Pro Lys Asn Ile Gly Glu Ile Lys Asp Lys Phe Glu Ala
 355 360 365
 Asn Lys Glu Lys Phe Lys Gln Ser Lys Asn Val Ser Glu Phe Ala Glu
 370 375 380
 Tyr Cys Arg Glu Cys Asn Pro Tyr Thr Ala Phe Asn Phe His Leu Asn
 385 390 395 400
 Ile Asn Asn Gly Leu Ser His Gln Phe Glu Lys Phe Val Pro Ile Met
 405 410 415
 Lys Glu Tyr Lys Glu Pro Lys Ile Thr Asp Asn Asp Leu Glu Ala Ile
 420 425 430
 Ser Thr Lys Glu Thr Gly Leu Ala Ser Gln Leu Ser Gly His Trp Phe
 435 440 445
 Phe Gln Leu Ser Leu Phe Asn Lys Thr Asn Phe Asn Pro Asn Lys Ile
 450 455 460
 Trp Ile Pro Leu Glu Phe Asn Lys Arg Ser Lys Ile Lys Phe Asp Lys
 465 470 475 480
 Asp Leu Glu Ile Tyr Phe Asp Ser His Glu Ser Phe Asn Ile Ser Lys
 485 490 495
 Lys Tyr Leu Gln Glu Ile Asp Gln Glu Ser Leu Lys Lys Ile Lys Gln
 500 505 510
 Ser Lys Asp Phe Phe Ser Ile Gln Lys Ile Glu Ser Lys His Asp Asn
 515 520 525
 Asn Asp Ile Leu Gln Leu Glu Phe Phe Glu Asn Asp Thr Ser Phe Leu
 530 535 540
 Phe Ala Lys Gly Ser Phe Ala Glu Ile Leu Glu Tyr Asn Met Gln Leu
 545 550 555 560
 Lys Ile Asp Ser Leu Ile Thr Lys Glu Phe Asn Lys Leu Leu Ala Ile
 565 570 575
 Val Gln Asp Ser Pro Gln Asp Ser Tyr Gln Leu Lys Ile Arg Val Arg
 580 585 590
 His Asn Asn Lys Leu Pro Arg Glu Lys Tyr Thr Glu His Glu Ile Lys

SUBSTITUTE SHEET (RULE 26)

1408

```

      595      600      605
Leu Glu Val Tyr Asp Cys Arg Lys Ser His Asp His Asn Glu Pro Ile
  610      615      620
Ile Leu Ser Gln Gln Ser Thr Gly Phe Gln Trp Ala Phe Asn Phe Met
  625      630      635      640
Phe Gly Phe Leu Tyr Asn Val Gly Ser His Phe Ser Phe Asn His Asn
      645      650      655
Ile Ile Tyr Val Met Asp Glu Pro Ala Thr His Leu Ser Val Pro Ala
      660      665      670
Arg Lys Glu Phe Arg Lys Phe Leu Lys Glu Tyr Ala His Lys Asn His
      675      680      685
Val Thr Phe Val Leu Ala Thr His Asp Pro Phe Leu Val Asp Thr Asp
      690      695      700
His Leu Asp Glu Ile Arg Ile Val Glu Lys Glu Thr Glu Gly Ser Val
  705      710      715      720
Ile Lys Asn His Phe Asn Tyr Pro Leu Asn Asn Ala Ser Lys Asp Ser
      725      730      735
Asp Ala Leu Asp Lys Ile Lys Arg Ser Leu Gly Val Gly Gln His Val
      740      745      750
Phe His Asn Pro Gln Lys His Arg Ile Ile Phe Val Glu Gly Ile Thr
      755      760      765
Asp Tyr Cys Tyr Leu Ser Ala Phe Lys Leu Tyr Leu Arg Tyr Lys Glu
      770      775      780
Tyr Lys Asp Asn Pro Ile Pro Phe Thr Phe Leu Pro Ile Ser Gly Leu
  785      790      795      800
Lys Asn Asp Ser Asn Asp Met Lys Glu Thr Ile Glu Lys Leu Cys Glu
      805      810      815
Leu Asp Asn His Pro Ile Val Leu Thr Asp Asp Asp Arg Lys Cys Val
      820      825      830
Phe Asn Gln Gln Ala Thr Ser Glu Arg Phe Lys Arg Ala Asn Glu Glu
      835      840      845
Met His Asp Pro Ile Thr Ile Leu Gln Leu Ser Asp Cys Asp Arg His
      850      855      860
Phe Lys Gln Ile Glu Asp Cys Phe Ser Ala Asn Asp Arg Asn Lys Tyr
  865      870      875      880
Ala Lys Asn Lys Gln Met Glu Leu Ser Met Ala Phe Lys Thr Arg Leu
      885      890      895
Leu Tyr Gly Gly Glu Asp Ala Ile Glu Lys Gln Thr Lys Arg Asn Phe
      900      905      910
Leu Lys Leu Phe Lys Trp Ile Ala Trp Ala Thr Asn Leu Ile Lys Asn
      915      920      925

```

(2) INFORMATION FOR SEQ ID NO:1882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1882

```

Gln Ala Leu Gly Ile Asn Met Cys Ser Lys Lys Ile Arg Asn Leu Ile
1           5           10           15

```

1409

```

Leu Cys Phe Gly Phe Ile Leu Ser Leu Cys Ala Glu Glu Asn Ile Thr
    20          25          30
Lys Glu Asn Met Thr Glu Thr Asn Thr Thr Glu Glu Asn Thr Pro Lys
    35          40          45
Asp Ala Pro Ile Leu Leu Glu Glu Lys Arg Ala Gln Thr Leu Glu Leu
    50          55          60
Lys Glu Glu Asn Glu Val Ala Lys Lys Ile Asp Glu Lys Ser Leu Leu
    65          70          75          80
Glu Glu Ile His Lys Lys Lys Arg Gln Leu Tyr Met Leu Lys Gly Glu
    85          90          95
Leu His Glu Lys Asn Glu Ser Ile Leu Phe Gln Gln Met Ala Lys Asn
    100          105          110
Lys Ser Gly Phe Phe Ile Gly Val Ile Leu Gly Asp Ile Gly Ile Asn
    115          120          125
Ala Asn Pro Tyr Glu Lys Phe Glu Leu Leu Ser Asn Ile Gln Ala Ser
    130          135          140
Pro Leu Leu Tyr Gly Leu Arg Ser Gly Tyr Gln Lys Tyr Phe Ala Asn
    145          150          155          160
Gly Ile Ser Ala Leu Arg Phe Tyr Gly Glu Tyr Leu Gly Gly Ala Met
    165          170          175
Lys Gly Phe Lys Ser Asp Ser Leu Ala Ser Tyr Gln Thr Ala Ser Leu
    180          185          190
Asn Ile Asp Leu Leu Met Asp Lys Pro Ile Asp Lys Glu Lys Arg Phe
    195          200          205
Ala Leu Gly Ile Phe Gly Gly Val Gly Val Gly Trp Asn Gly Met Tyr
    210          215          220
Gln Asn Leu Lys Glu Ile Arg Gly Tyr Ser Gln Pro Asn Ala Phe Gly
    225          230          235          240
Leu Val Leu Asn Leu Gly Val Ser Met Thr Leu Asn Leu Lys His Arg
    245          250          255
Phe Glu Leu Ala Leu Lys Met Pro Pro Leu Lys Glu Thr Ser Gln Thr
    260          265          270
Phe Leu Tyr Tyr Phe Lys Ser Thr Asn Ile Tyr Tyr Ile Ser Tyr Asn
    275          280          285
Tyr Leu Leu
    290

```

(2) INFORMATION FOR SEQ ID NO:1883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1883

```

Arg Phe Phe Arg Lys His Arg Val Ile Ser Met Lys Glu Ile Val Thr
  1          5          10          15
Ile Glu Asn Val Ser Phe Asn Tyr His Asn Arg Ala Ile Phe Lys Asp
    20          25          30
Phe Asn Leu Ser Ile Gln Glu Gly Asp Phe Leu Cys Val Leu Gly Glu
    35          40          45
Ser Gly Ser Gly Lys Ser Thr Leu Leu Gly Leu Ile Leu Gly Leu Leu

```

SUBSTITUTE SHEET (RULE 26)

1410

```

      50              55              60
Lys Pro Ser Leu Gly Ser Val Lys Ile Phe Asn Glu Thr Leu Ser Asn
65              70              75              80
Asn Ala Phe Leu Arg Gln Lys Ile Gly Tyr Ile Ala Gln Gly Asn Ser
      85              90              95
Leu Phe Pro His Leu Asn Ala Leu Gln Asn Met Thr Phe Cys Leu Asn
      100             105             110
Leu Gln Gly Ile Asn Lys Gln Ala Ala Gln Lys Glu Ala Lys Ala Leu
      115             120             125
Ala Leu Lys Met Gly Leu Asp Glu Ser Leu Met Asp Lys Phe Pro Asn
      130             135             140
Glu Leu Ser Gly Gly Gln Ala Gln Arg Val Gly Ile Ile Arg Gly Ile
145             150             155             160
Ile His Arg Pro Glu Leu Ile Leu Leu Asp Glu Pro Phe Ser Ala Leu
      165             170             175
Asp Ser Leu Asn Arg Lys Asn Leu Gln Asp Leu Ile Lys Glu Ile His
      180             185             190
Gln Asn Ser Cys Ala Thr Phe Ile Met Val Thr His Asp Glu Asn Glu
      195             200             205
Ala Gln Lys Leu Ala Thr Lys Thr Leu Glu Ile Lys Ala Leu Lys Gln
      210             215             220
Glu Gln
225

```

(2) INFORMATION FOR SEQ ID NO:1884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1884

```

Met Ala Asp Leu Leu Ser Ser Leu Lys Asn Leu Ser Ser Ser Ser Gly
1              5              10              15
Val Tyr Gln Tyr Phe Asp Lys Asn Arg Gln Leu Leu Tyr Ile Gly Lys
      20              25              30
Ala Lys Asn Leu Lys Lys Arg Ile Lys Ser Tyr Phe Ser Val Arg Asn
      35              40              45
Asn Glu Ile Thr Pro Asn Pro Arg Thr Ser Leu Arg Val Gln Met Met
      50              55              60
Val Lys Gln Ile Ala Phe Leu Glu Thr Ile Leu Val Glu Asn Glu Gln
65              70              75              80
Asp Ala Leu Ile Leu Glu Asn Ser Leu Ile Lys Gln Leu Lys Pro Lys
      85              90              95
Tyr Asn Ile Leu Leu Arg Asp Asp Lys Thr Tyr Pro Tyr Ile Tyr Met
      100             105             110
Asp Phe Ser Ile Asp Phe Pro Ile Pro Leu Ile Thr Arg Lys Ile Leu
      115             120             125
Lys Gln Pro Gly Val Lys Tyr Phe Gly Pro Phe Thr Ser Gly Ala Lys
      130             135             140
Asp Ile Leu Asp Ser Leu Tyr Glu Leu Leu Pro Leu Val Gln Lys Lys
145             150             155             160

```

SUBSTITUTE SHEET (RULE 26)

1411

Asn Cys Ile Lys Asp Lys Lys Ala Cys Met Phe Tyr Gln Ile Glu Arg
 165 170 175
 Cys Lys Ala Pro Cys Glu Asp Lys Ile Thr Lys Glu Glu Tyr Leu Lys
 180 185 190
 Ile Ala Lys Glu Cys Leu Glu Met Ile Glu Asn Lys Asp Arg Leu Ile
 195 200 205
 Lys Glu Leu Glu Leu Lys Met Glu Arg Leu Ser Ser Asn Leu Arg Phe
 210 215 220
 Glu Glu Ala Leu Ile Tyr Arg Asp Arg Ile Ala Lys Ile Gln Lys Ile
 225 230 235 240
 Ala Pro Phe Thr Cys Met Asp Leu Ala Lys Leu Tyr Asp Leu Asp Ile
 245 250 255
 Phe Ala Phe Tyr Gly Gly Asn Asn Lys Ala Val Leu Val Lys Met Phe
 260 265 270
 Met Arg Gly Gly Lys Ile Ile Ser Ser Ala Phe Glu Lys Ile His Ser
 275 280 285
 Leu Asn Gly Phe Asp Thr Asp Glu Ala Met Lys Gln Ala Ile Ile Asn
 290 295 300
 His Tyr Gln Ser His Leu Pro Leu Met Pro Glu Gln Ile Leu Leu Ser
 305 310 315 320
 Ala Cys Ser Asn Glu Thr Leu Lys Glu Leu Gln Glu Phe Ile Ser His
 325 330 335
 Gln Tyr Ser Lys Lys Ile Ala Leu Ser Ile Pro Lys Lys Gly Asp Lys
 340 345 350
 Leu Ala Leu Ile Glu Ile Ala Met Lys Asn Ala Gln Glu Ile Phe Ser
 355 360 365
 Gln Glu Lys Thr Ser Asn Glu Asp Arg Ile Leu Glu Glu Ala Arg Ser
 370 375 380
 Leu Phe Asn Leu Glu Cys Val Pro Tyr Arg Val Glu Ile Phe Asp Thr
 385 390 395 400
 Ser His His Ser Asn Ser Gln Cys Val Gly Gly Met Val Val Tyr Glu
 405 410 415
 Asn Asn Ala Phe Gln Lys Asp Ser Tyr Arg Arg Tyr His Leu Lys Gly
 420 425 430
 Ser Asn Glu Tyr Asp Gln Met Ser Glu Leu Leu Thr Arg Arg Ala Leu
 435 440 445
 Asp Phe Ala Lys Glu Pro Pro Pro Asn Leu Trp Val Ile Asp Gly Gly
 450 455 460
 Arg Ala Gln Leu Asn Ile Ala Leu Glu Ile Leu Lys Ser Ser Gly Ser
 465 470 475 480
 Phe Val Glu Val Ile Ala Ile Ser Lys Glu Lys Arg Asp Ser Lys Ala
 485 490 495
 Tyr Arg Ser Lys Gly Gly Ala Lys Asp Ile Ile His Thr Ile Ser His
 500 505 510
 Thr Phe Lys Leu Leu Pro Ser Asp Lys Arg Leu Gln Trp Val Gln Lys
 515 520 525
 Leu Arg Asp Glu Ser His Arg Tyr Ala Ile Asn Phe His Arg Ser Thr
 530 535 540
 Lys Leu Lys Asn Met Lys Gln Ile Ala Leu Leu Lys Glu Lys Gly Ile
 545 550 555 560
 Gly Glu Ala Ser Val Lys Lys Leu Leu Asp Tyr Phe Gly Ser Phe Glu
 565 570 575
 Ala Ile Glu Lys Ala Ser Asp Gln Glu Lys Asn Ala Val Leu Lys Lys
 580 585 590
 Arg Lys

(2) INFORMATION FOR SEQ ID NO:1885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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1412

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1885

```

Arg Lys Asn Met Lys Lys Arg Leu Asn Ile Gly Leu Val Gly Leu Gly
1      5      10      15
Cys Val Gly Ser Thr Val Ala Lys Ile Leu Gln Glu Asn Gln Glu Ile
20     25     30
Ile Lys Asp Arg Ala Gly Val Glu Ile Lys Ile Lys Lys Ala Val Val
35     40     45
Arg Asp Val Lys Lys His Lys Gly Tyr Ala Phe Glu Ile Ser Asp Asp
50     55     60
Leu Glu Ser Val Ile Glu Asp Lys Gly Ile Asp Ile Val Val Glu Leu
65     70     75     80
Met Gly Gly Val Glu Ala Pro Tyr Leu Leu Ala Lys Lys Thr Leu Ala
85     90     95
Lys Gln Lys Ala Phe Val Thr Ala Asn Lys Ala Met Leu Ala Tyr His
100    105    110
Arg Tyr Glu Leu Glu Gln Ile Ala Lys Asn Thr Pro Ile Gly Phe Glu
115    120    125
Ala Ser Val Cys Gly Gly Ile Pro Ile Ile Lys Ala Leu Lys Asp Gly
130    135    140
Leu Ser Ala Asn His Ile Leu Ser Phe Lys Gly Ile Leu Asn Gly Thr
145    150    155    160
Ser Asn Tyr Ile Leu Ser Gln Met Phe Lys Asn Gln Ala Ser Phe Lys
165    170    175
Asp Ala Leu Lys Asp Ala Gln His Leu Gly Tyr Ala Glu Leu Asn Pro
180    185    190
Glu Phe Asp Ile Lys Gly Ile Asp Ala Ala His Lys Leu Leu Ile Leu
195    200    205
Ala Ser Leu Ala Tyr Gly Ile Asp Ala Lys Leu Glu Glu Ile Leu Ile
210    215    220
Glu Gly Ile Glu Lys Ile Glu Pro Asp Asp Met Glu Phe Ala Lys Glu
225    230    235    240
Phe Gly Tyr Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Asp
245    250    255
Cys Ile Glu Leu Arg Val His Pro Ser Met Ile Lys Asn Glu Cys Met
260    265    270
Leu Ser Lys Val Asp Gly Val Met Asn Ala Ile Ser Val Ile Gly Asp
275    280    285
Lys Val Gly Glu Thr Leu Tyr Tyr Gly Ala Gly Ala Gly Gly Glu Pro
290    295    300
Thr Ala Ser Ala Val Ile Ser Asp Ile Ile Glu Ile Ala Arg Lys Lys
305    310    315    320
Ser Ser Leu Met Leu Gly Phe Glu Thr Pro Gln Lys Leu Pro Leu Lys
325    330    335
Pro Lys Glu Glu Ile Gln Cys Ala Tyr Tyr Ala Arg Leu Leu Val Ser
340    345    350
Asp Glu Lys Gly Val Phe Ser Gln Ile Ser Ala Ile Leu Ala Gln Asn
355    360    365
Asp Ile Ser Leu Asn Asn Val Leu Gln Lys Glu Ile Pro Gln Ser Asn
370    375    380
Lys Ala Lys Ile Leu Phe Ser Thr His Thr Thr Asn Glu Lys Ser Met
385    390    395    400
Leu Asn Ala Leu Lys Glu Leu Glu Asn Leu Gln Ser Val Leu Asp Thr
405    410    415

```

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1413

Pro Lys Met Ile Arg Leu Glu Asn
420

(2) INFORMATION FOR SEQ ID NO:1886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 326 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1886

```

Ser Arg Phe Lys Arg Ala Ile Glu Gln Ala Phe Arg Leu Val Ala Met
1          5          10          15
Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu Ser Ala Gly
20          25          30
Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu Phe Glu Lys
35          40          45
Gly Met Pro Gly Gly Gln Ile Thr Gly Ser Ser Glu Ile Glu Asn Tyr
50          55          60
Pro Gly Val Lys Glu Val Val Ser Gly Leu Asp Phe Met Gln Pro Trp
65          70          75          80
Gln Glu Gln Cys Phe Arg Phe Gly Leu Lys His Glu Met Thr Ala Ile
85          90          95
Gln Arg Val Ser Lys Lys Gly Ser His Phe Val Ile Leu Ala Glu Asp
100          105          110
Gly Lys Thr Phe Glu Ala Lys Ser Val Ile Ile Ala Thr Gly Gly Ser
115          120          125
Pro Lys Arg Thr Gly Ile Lys Gly Glu Ser Glu Tyr Trp Gly Lys Gly
130          135          140
Val Ser Thr Cys Ala Thr Cys Asp Gly Phe Phe Tyr Lys Asn Lys Glu
145          150          155          160
Val Ala Val Leu Gly Gly Gly Asp Thr Ala Val Glu Glu Ala Ile Tyr
165          170          175
Leu Ala Asn Ile Cys Lys Lys Val Tyr Leu Ile His Arg Arg Asp Gly
180          185          190
Phe Arg Cys Ala Pro Ile Thr Leu Glu His Ala Lys Asn Asn Ser Lys
195          200          205
Ile Glu Phe Leu Thr Pro Tyr Val Val Glu Glu Ile Lys Gly Asp Ala
210          215          220
Ser Gly Val Ser Ser Leu Ser Ile Lys Asn Thr Ala Thr Asn Glu Lys
225          230          235          240
Arg Glu Leu Val Val Pro Gly Leu Phe Ile Phe Val Gly Tyr Asp Val
245          250          255
Asn Asn Ala Val Leu Lys Gln Glu Asp Asn Ser Met Leu Cys Glu Cys
260          265          270
Asp Glu Tyr Gly Ser Ile Val Val Asp Phe Ser Met Lys Thr Asn Val
275          280          285
Gln Gly Leu Phe Ala Ala Gly Asp Ile Arg Ile Phe Ala Pro Lys Gln
290          295          300
Val Val Cys Ala Ala Ser Asp Gly Ala Thr Ala Ala Leu Ser Val Ile
305          310          315          320
Ser Tyr Leu Glu His His

```

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(2) INFORMATION FOR SEQ ID NO:1887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1887

```

Lys Leu Trp Glu Phe Ser Leu Arg Val Phe Ile Ile Ser Leu Asn Gln
1      5      10      15
Lys Val Cys Asp Lys Phe Gly Leu Val Phe Arg Asp Thr Thr Thr Leu
20      25      30
Leu Asn Asn Ile Asn Ala Thr His Gln Ala Gln Ile Phe Asp Ala
35      40      45
Ile Tyr Ser Lys Thr Phe Glu Gly Gly Leu His Pro Leu Val Lys Lys
50      55      60
His Leu His Pro Tyr Phe Ile Thr Gln Asn Ile Lys Asp Met Gly Ile
65      70      75      80
Ala Thr Ser Leu Ile Ser Glu Val Ser Lys Phe Tyr Tyr Ala Leu Lys
85      90      95
Tyr His Ala Lys Phe Met Ser Leu Gly Glu Leu Gly Cys Tyr Ala Ser
100     105     110
His Tyr Ser Leu Trp Gln Lys Cys Ile Glu Leu Asn Glu Ala Ile Cys
115     120     125
Ile Leu Glu Asp Asp Ile Thr Leu Lys Glu Asp Phe Lys Glu Gly Leu
130     135     140
Asp Phe Leu Glu Lys His Ile Gln Glu Leu Gly Tyr Ala Arg Leu Met
145     150     155     160
His Leu Leu Tyr Asp Ala Ser Val Lys Ser Glu Pro Leu Asn His Glu
165     170     175
Asn Gln Glu Ile Gln Glu Arg Val Gly Ile Ile Lys Ala Tyr Ser His
180     185     190
Gly Val Gly Thr Gln Gly Tyr Val Ile Thr Pro Lys Ile Ala Lys Val
195     200     205
Phe Leu Lys His Ser Arg Lys Trp Val Val Pro Val Asp Thr Ile Met
210     215     220
Asp Ala Thr Phe Ile His Gly Val Lys Asn Leu Val Leu Gln Pro Phe
225     230     235     240
Val Ile Ala Asp Asp Glu Gln Ile Ser Thr Ile Ala Arg Lys Glu Glu
245     250     255
Pro Tyr Ser Pro Lys Ile Ala Leu Met Arg Glu Leu His Phe Lys Phe
260     265     270
Leu Lys Trp Trp Gln Phe Val
275

```

(2) INFORMATION FOR SEQ ID NO:1888:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

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(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1888

Gly	Asp	Phe	Ile	Ile	Ser	Asn	Ile	Ser	Ile	His	Pro	Lys	Thr	Met	Phe
1			5					10						15	
Lys	Asn	Ala	Leu	Asn	Ile	Gln	Asp	Phe	Ser	Phe	Lys	Asn	His	Thr	Ser
		20					25					30			
Thr	Ala	Ile	Ile	Gly	Thr	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Ile	Asn
	35					40					45				
Thr	Ile	Leu	Gly	Ile	Arg	Ser	Asp	Tyr	Asn	Phe	Lys	Ala	Gln	Asn	Asn
50					55					60					
Asn	Ile	Pro	Tyr	His	Asp	Asn	Val	Ile	Pro	Gln	Arg	Lys	Gln	Leu	Gly
65			70					75						80	
Val	Val	Ser	Asn	Leu	Phe	Asn	Tyr	Pro	Pro	Gly	Leu	Asn	Ala	Asn	Asp
			85					90						95	
Leu	Phe	Lys	Phe	Tyr	Gln	Phe	Phe	His	Lys	Asn	Cys	Thr	Leu	Asp	Leu
		100					105						110		
Phe	Glu	Lys	Asn	Leu	Leu	Asn	Lys	Thr	Tyr	Glu	His	Leu	Ser	Asp	Gly
		115				120						125			
Gln	Lys	Gln	Arg	Leu	Lys	Ile	Asp	Leu	Ala	Leu	Ser	His	His	Pro	Gln
130					135						140				
Leu	Val	Ile	Met	Asp	Glu	Pro	Glu	Thr	Ser	Leu	Glu	Gln	Asn	Ala	Leu
145				150					155						160
Ile	Arg	Leu	Ser	Asn	Leu	Ile	Ser	Leu	Arg	Asn	Thr	Gln	Gln	Leu	Thr
			165					170						175	
Ser	Ile	Ile	Ala	Thr	His	Asp	Pro	Ile	Val	Leu	Asp	Ser	Cys	Glu	Trp
		180					185						190		
Val	Leu	Leu	Leu	Lys	Asn	Gly	Asn	Ile	Ala	Gln	Tyr	Lys	Pro	Leu	Asn
		195				200						205			
Ser	Ile	Leu	Lys	Ser	Val	Ala	Lys	Thr	Phe	Asn	Phe	Lys	Glu	Lys	Pro
210				215							220				
Thr	Thr	Lys	Asp	Leu	Leu	Ala	Leu	Leu	Lys	Asp	Ile				
225				230						235					

(2) INFORMATION FOR SEQ ID NO:1889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...113

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1889

```

Ile Tyr Ser His Leu Ala Pro Ile Met His Tyr Gln Leu Thr Ser Phe
1           5           10           15
Asn Ile Ile Gln Asp Leu Phe Ile Thr Cys His Val Leu Arg Ile Lys
20           25           30
Met Arg Val Phe Val Cys Phe Leu Gly Val Phe Val Ser Asn Gly Leu
35           40           45
Ala Arg Phe Gly Tyr Val Val Leu Ile Pro Leu Leu Ile Leu Ser Gly
50           55           60
Ser Leu Thr Pro His Gln Ser Phe Gln Leu Gly Ile Ala Val Leu Met
65           70           75           80
Gly Tyr Val Phe Gly Ser Phe Leu Ile Gln Phe Leu Ser Pro Leu Met
85           90           95
Ser Leu Glu Ser Ile Ala Lys Ile Ser Phe Lys Leu Ile Thr Leu Ser
100          105          110
Phe

```

(2) INFORMATION FOR SEQ ID NO:1890:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1890

```

Ser Met Gly Gly Phe Thr Ser Ile Trp His Trp Val Ile Val Leu Leu
1           5           10           15
Val Ile Val Leu Leu Phe Gly Ala Lys Lys Ile Pro Glu Leu Ala Lys
20           25           30
Gly Leu Gly Ser Gly Ile Lys Asn Phe Lys Lys Ala Val Lys Asp Asp
35           40           45
Glu Glu Glu Ala Lys Asn Glu Leu Lys Thr Leu Asp Ala Gln Ala Thr
50           55           60
Gln Thr Lys Val His Glu Thr Ser Glu Ile Lys Ser Lys Gln Glu Ser
65           70           75           80

```

(2) INFORMATION FOR SEQ ID NO:1891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...267

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1891

```

Arg Lys Thr Asn His Lys Arg Leu Ile Ser Val Thr Lys Gly Tyr Leu
1          5          10          15
Met Gly Ala Ile Leu Ser Ile Leu Lys Leu Glu Ile Lys Ser Tyr Leu
          20          25          30
Thr Asn Thr Ser Ala Leu Phe Trp Thr Phe Ile Tyr Pro Ile Leu Met
          35          40          45
Leu Leu Leu Leu Ile Phe Val Phe Ser Lys Asn Thr Thr Glu Ile Phe
          50          55          60
Tyr Phe Asn Asn Ile Ile Gly Leu Met Gly Leu Leu Ile Ile Ser Ser
65          70          75          80
Ala Ile Phe Gly Leu Thr Gln Ala Ile Thr Ser Ser Arg Ser His Asn
          85          90          95
Ile Phe Leu Phe Tyr Met Leu Ser Pro Ala Thr Phe Lys Gln Ile Thr
          100         105         110
Leu Ala Leu Ile Ala Ser Arg Leu Ile Val Val Ile Leu Tyr Ala Phe
          115         120         125
Ile Phe Ile Val Leu Ser Phe Tyr Ala Leu Asn Ile Ile Thr Ile Leu
          130         135         140
Asn Phe Lys Ala Leu Ile Leu Gly Phe Ile Ser Ile Phe Ser Ser Ala
145         150         155         160
Leu Phe Cys Phe Cys Leu Ala Ile Phe Val Ala Arg Ile Phe Gln Asn
          165         170         175
Glu Gln Ser Ile Leu Gly Phe Cys Asn Ile Ile Asn Leu Tyr Ala Leu
          180         185         190
Met Ser Cys Asn Val Phe Val Pro Leu Glu Tyr Leu Pro Asn Ile Gly
          195         200         205
Gln Leu Phe Ile Lys Thr Ser Ile Phe Tyr Tyr Leu Asn Gln Leu Leu
          210         215         220
Ile Lys Ala Phe Gln Gly Ile Asp Thr Ile Leu Val Leu Ala Thr Ser
225         230         235         240
Thr Phe Phe Ile Ile Gly Gly Ile Ile Leu Phe Leu Leu Ser Ala Asn
          245         250         255
Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg
          260         265

```

(2) INFORMATION FOR SEQ ID NO:1892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 272 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1892

```

Arg Lys Gln Glu Met Lys Lys Leu Leu Leu Leu Glu His Lys Ile

```

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```

1           5           10           15
Val Lys Ile Gly Leu Ile Ile Val Ile Val Leu Val Gly Phe Phe Leu
20           25           30
Phe Tyr Glu Gln Glu Ile Lys Glu Lys Ala Val Asn Val Ser Gln Gly
35           40           45
Lys Phe Pro Thr Ser Ser Tyr Leu Phe Gln Ala Tyr Glu Gly Ile Lys
50           55           60
Asn Lys Ile Asp Thr Ile Asn Gln Val Lys Pro Asn Asp Glu Thr Lys
65           70           75           80
Ser Val Asn Glu Asn Ile Glu Lys Thr Gln Lys Asp Leu Asp Asp Phe
85           90           95
Asn Ala Leu Val Gln Lys Leu Pro Asn Leu Pro Lys Asp Phe Asn Lys
100          105          110
Thr Leu Ile Lys Pro Gln Ser Pro Phe Phe Asn Tyr Asn Thr Ala Asn
115          120          125
Glu Asp Glu Lys Asn Arg Leu Val Ile Leu Ala Ser Arg Ile Ser Ser
130          135          140
Gln Lys Glu Thr Gln Pro Ile Ser Ile Lys Asn Ser Val Ser His
145          150          155          160
Ile Lys Ser Lys Glu Lys Arg Glu Leu Glu Lys Glu Trp Ala Lys Pro
165          170          175
Ser Val Ser Phe Gly Ser Phe Ser Leu Leu Ser Ser Ser Ser Phe
180          185          190
Ser Ser Phe Glu Val Ser Phe Leu Ser Arg Gly Ile Gly Leu Asp Cys
195          200          205
Glu Lys Leu Lys Ser Phe Leu Lys Ala Phe Ser Ser Ser Leu Phe Ser
210          215          220
Leu Leu Ser Ser Leu Phe Cys His Pro Leu Ser Leu Phe Cys Ser Leu
225          230          235          240
Ile Gly Leu Ile Phe Cys Phe Ser Lys Phe Ser Arg Glu Leu Val Asn
245          250          255
Ala Ser Asn Asn Ser Leu Glu Phe Ser Ser Leu Ser Arg Leu Gly Ser
260          265          270

```

(2) INFORMATION FOR SEQ ID NO:1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1893

```

Lys Ile Phe Lys Lys Ala Leu Arg His Lys Met Glu Lys Val Cys Val
1           5           10           15
Ser Ala Trp Gly Leu Pro Lys Ile Leu Glu Glu Arg Leu Lys Glu Lys
20           25           30
Tyr Gly Asp Asp Trp Glu Lys His Val Lys Ala Lys Ala Ile Asn Glu
35           40           45
Glu Glu Leu Glu Glu Gln Val Lys Ala Lys Ala Lys Glu Gln Gln Lys
50           55           60
Thr Gln Arg Glu Lys Thr Leu Asn Gly Phe Leu Lys Lys Val Gly Leu
65           70           75           80

```


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Lys Lys Arg Asp Met Leu Gln Ser Thr Met Leu Phe Asp Glu Val Lys
 85 90 95
 Glu Ala Asp Val Leu Phe Gln Ala Glu Arg Lys Ile Gly Asp Trp Ile
 100 105 110
 Phe Ser Ser Ala Val Phe Phe Phe Ala Leu Ala Leu Ile Glu Ala Ile
 115 120 125
 Ile Ile Val Cys Leu Leu Pro Leu Lys Glu Lys Val Pro Tyr Leu Val
 130 135 140
 Thr Phe Ser Asn Ala Thr Gln Asn Phe Ala Ile Val Gln Arg Ala Asp
 145 150 155 160
 Lys Ser Ile Arg Ala Asn Gln Ala Leu Val Arg Gln Leu Val Ala Ser
 165 170 175
 Tyr Val Asn Asn Arg Glu Asn Ile Ser Ser Ile Lys Glu Gln Asn Glu
 180 185 190
 Ile Ala His Glu Thr Ile Arg Leu Gln Ser Ala Phe Glu Val Trp Asp
 195 200 205
 Phe Phe Glu Lys Leu Val Ser Tyr Glu His Ser Ile Tyr Thr Asn Ile
 210 215 220
 Asn Leu Thr Arg Lys Ile Ser Ile Ile Asn Ile Ala Leu Ile Ser Lys
 225 230 235 240
 Thr Gln Ala Asn Ile Glu Ile Ser Ala Gln Leu Phe His Lys Glu Lys
 245 250 255
 Leu Glu Ser Glu Lys Arg Tyr Arg Ile Ile Met Thr Phe Glu Phe Glu
 260 265 270
 Pro Ile Glu Ile Asp Thr Lys Ser Val Pro Leu Asn Pro Thr Gly Phe
 275 280 285
 Ile Val Thr Gly Tyr Asp Val Thr Glu Ile Ala Ile Leu Lys Asp Leu
 290 295 300
 Asp Glu Lys Asn Lys Val Lys Asp Asp Gly Val Lys Ser Arg Ile Ile
 305 310 315 320
 His Val Glu Lys Lys Asp Pro His Met Ser Gln Tyr Lys Asp Val Lys
 325 330 335
 Glu Gln

(2) INFORMATION FOR SEQ ID NO:1894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1894

Val Val Val Ile Arg Leu Val Leu Asn Met Leu Thr Cys Gln Ile Ser
 1 5 10 15
 Tyr Ile Arg Ile Ser Tyr Leu Val Ser Val Ser Asp Phe Val Ile Cys
 20 25 30
 Lys Glu Arg Phe Met Asp Glu Ile Lys Thr Leu Leu Val Asp Phe Phe
 35 40 45
 Pro Gln Ala Lys His Phe Gly Ile Ile Leu Ile Lys Ala Ile Val Val
 50 55 60
 Phe Cys Ile Gly Phe Tyr Phe Ser Phe Phe Leu Arg Asn Lys Thr Met

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```

65          70          75          80
Lys Leu Leu Ser Lys Lys Asp Glu Ile Leu Ala Asn Phe Val Ala Gln
      85          90          95
Val Thr Phe Ile Leu Ile Leu Ile Ile Thr Thr Ile Ile Ala Leu Ser
      100         105         110
Thr Leu Gly Val Gln Thr Thr Ser Ile Ile Thr Val Leu Gly Thr Val
      115         120         125
Gly Ile Ala Val Ala Leu Ala Leu Lys Asp Tyr Leu Ser Ser Ile Ala
      130         135         140
Gly Gly Ile Ile Leu Ile Ile Leu His Pro Phe Lys Lys Gly Asp Ile
145          150         155         160
Ile Glu Ile Ser Gly Leu Glu Gly Lys Val Glu Ala Leu Asn Phe Phe
      165         170         175
Asn Thr Ser Leu Arg Leu His Asp Gly Arg Leu Ala Val Leu Pro Asn
      180         185         190
Arg Ser Val Ala Asn Ser Asn Ile Ile Asn Ser Asn Asn Thr Ala Cys
      195         200         205
Arg Arg Ile Glu Trp Val Cys Gly Val Gly Tyr Gly Ser Asp Ile Glu
210          215         220
Leu Val His Lys Thr Ile Lys Asp Val Ile Asp Gly Met Glu Lys Ile
225          230         235         240
Asp Lys Asn Met Pro Thr Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser
      245         250         255
Ser Leu Asn Phe Thr Ile Arg Val Trp Ala Lys Ile Glu Asp Gly Ile
260          265         270
Phe Asn Val Arg Ser Glu Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp
275          280         285
Ala Asn Arg Ile Glu Ile Pro Phe Asn Lys Leu Asp Ile Ser Ile Asn
290          295         300
Lys Gln Asp Ser Ser Lys
305          310

```

(2) INFORMATION FOR SEQ ID NO:1895:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1895

```

Ser Lys Arg Thr Gln Gln Thr Phe Phe Leu Phe Ile Asp Glu Thr Lys
1          5          10          15
Asp Tyr Ile Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu
      20         25         30
Ala Gln Ala Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys
      35         40         45
Ile Ser Gln Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile
50          55         60
Gly Asn Leu Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu
65          70         75         80
Leu Ile Glu Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu
      85         90         95

```

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```

His Asn Thr Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val
      100      105      110
Thr Asn Ala Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys
      115      120      125
Asn Tyr Phe Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser
      130      135      140
Met Ile Leu Lys Lys Gln Thr Lys Lys Leu Ile Arg Lys Ser Ile
      145      150      155

```

(2) INFORMATION FOR SEQ ID NO:1896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
 (B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1896

```

Leu Leu Lys Asn Ile Asp Glu Lys Lys Leu Ser Val Ser Lys Val Asn
1      5      10      15
Glu Lys Arg His Met Asp Phe Lys Lys Cys Pro Asn Phe Glu Lys Lys
      20      25      30
Cys Ala Phe Leu Cys Phe Ser Asn Leu Val Leu Leu Ile Glu Ile His
      35      40      45
Ser Lys Gly Leu His Met Gln Lys Lys Lys Pro Lys Asn Pro Gln Pro
      50      55      60
Asn Leu Phe Ser Ile Leu Asp Lys Gly Asp Val Ala Thr Asn Asn Pro
      65      70      75      80
Val Glu Glu Ser Asp Lys Ala Asn Lys Ile Gln Glu Pro Leu Pro Tyr
      85      90      95
Val Val Lys Thr Gln Ile Asn Lys Ala Ser Met Ile Ser Arg Asp Pro
      100      105      110
Ile Glu Trp Ala Lys Tyr Leu Ser Phe Glu Lys Arg Val Tyr Lys Asp
      115      120      125
Asn Ser Lys Glu Asp Val Asn Phe Phe Ala Asn Gly Glu Ile Lys Glu
      130      135      140
Ser Ser Arg Val Tyr Glu Ala Asn Lys Glu Gly Phe Glu Arg Arg Ile
      145      150      155      160
Thr Lys Arg Tyr Asp Leu Ile Asp Arg Asn Ile Asp Arg Asn Arg Glu
      165      170      175
Phe Phe Ile Lys Glu Ile Glu Ile Leu Thr His Thr Asn Ser Leu Lys
      180      185      190
Glu Leu Lys Glu Gln Gly Leu Glu Ile Gln Leu Thr His His Asn Glu
      195      200      205
Thr His Lys Lys Ala Leu Glu Asn Gly Asn Glu Ile Val Lys Glu Tyr
      210      215      220
Asp His Leu Lys Asp Ile Tyr Gln Glu Val Glu Arg Thr Lys Asp Gly
      225      230      235      240
Gly Leu Val Arg Glu Ile Ile Pro Ser Ile Ser Ser Ala Glu Tyr Phe
      245      250      255
Thr Leu

```

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(2) INFORMATION FOR SEQ ID NO:1897:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1897

TATACCATGG TGGGCGCTAA

20

(2) INFORMATION FOR SEQ ID NO:1898:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1898

ATGAATTCGA GTAAGGATTT TTG

23

(2) INFORMATION FOR SEQ ID NO:1899:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1899

TTAACCATGG TGAAAAGCGA TA

22

(2) INFORMATION FOR SEQ ID NO:1900:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1900

TAGAATTCGC ATAACGATCA ATC

23

(2) INFORMATION FOR SEQ ID NO:1901:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1901

ATATCCATGG TGAGTTTGAT GA

22

(2) INFORMATION FOR SEQ ID NO:1902:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1902

ATGAATTCAA TTTTATTATT TGCCA

25

(2) INFORMATION FOR SEQ ID NO:1903:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1903

AATTCCATGG TGGGGGCTAT G

21

(2) INFORMATION FOR SEQ ID NO:1904:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1904

ATGAATTCTC GATAGCCAAA ATC

23

(2) INFORMATION FOR SEQ ID NO:1905:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1905

AATTCCATGG TGCATAACTT CCATT

25

(2) INFORMATION FOR SEQ ID NO:1906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1906

AAGAATTCTC TAGCATCCAA ATGGA

25

(2) INFORMATION FOR SEQ ID NO:1907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...24
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1907

ATTTCATGG TCATGTCTCA TATT

24

(2) INFORMATION FOR SEQ ID NO:1908:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1908

ATGAATTC CA TCTTTTATTC CAC

23

(2) INFORMATION FOR SEQ ID NO:1909:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...27
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1909

AACCATGGTG ATTTTAAGCA TTGAAAG

27

(2) INFORMATION FOR SEQ ID NO:1910:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1910

AAGAATTCCA CTCAAATTT TTAAACAG

28

(2) INFORMATION FOR SEQ ID NO:1911:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1911

GATCATCCAT ATGTTATCTT CTAAT

25

(2) INFORMATION FOR SEQ ID NO:1912:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1912

TGAATTCAAC CATTTTAACC CTG

23

(2) INFORMATION FOR SEQ ID NO.:1913

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1913

TATACCATGG TGAAATTTTT TCTTTTA

27

(2) INFORMATION FOR SEQ ID NO:1914:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1914

AGAATTCAAT TCGTCTTGT AAAAG

25

(2) INFORMATION FOR SEQ ID NO:1915:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

1429

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1915

TATACCATGG TGATGGACAA ACTC

24

(2) INFORMATION FOR SEQ ID NO:1916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1916

ATGAATTCCC ACTTGGGGCG ATA

23

(2) INFORMATION FOR SEQ ID NO:1917:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1917

TTATGGATCC AAACCAATTA AAAC

25

(2) INFORMATION FOR SEQ ID NO:1918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1918

TATCTCGAGT TATAGAGAAG GGC

23

(2) INFORMATION FOR SEQ ID NO:1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1919

TTAACCATGG TGAAAAGCGA TA

22

(2) INFORMATION FOR SEQ ID NO:1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

1431

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...24
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1920

TAGAATTCGC CTCTAAACT TTAG

24

(2) INFORMATION FOR SEQ ID NO:1921:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1921

TTAACCATGG TGAAAAGCGA TA

22

(2) INFORMATION FOR SEQ ID NO:1922:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1922

TAGAATTCGC ATAACGATCA ATC

23

1432

(2) INFORMATION FOR SEQ ID NO:1923:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1923

ATATCCATGG TGAGTTTGAT GA

22

(2) INFORMATION FOR SEQ ID NO:1924:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...25

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1924

ATGAATTCAA TTTTATTATT TGCCA

25

(2) INFORMATION FOR SEQ ID NO:1925:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...23

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1925

AATTCCATGG CTATCCAAAT CCG

23

(2) INFORMATION FOR SEQ ID NO:1926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1926

ATGAATTCGC CAAAATCGTA GTATT

25

(2) INFORMATION FOR SEQ ID NO:1927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1927

GATACCATGG AATTTATGAA AAAG

24

(2) INFORMATION FOR SEQ ID NO:1928:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1928

TGAATTCGAA AAAGTGTAGT TATAC

25

(2) INFORMATION FOR SEQ ID NO::1929

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1929

CCCTTCATTT TAGAAATCG

19

(2) INFORMATION FOR SEQ ID NO:1930:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1930

ATTTC AACCA ATTCAATGCG

20

(2) INFORMATION FOR SEQ ID NO:1931:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1931

GCCCTTTTG ATTGAAGCT

20

(2) INFORMATION FOR SEQ ID NO:1932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1932

TCGCTCCAAG ATACCAAGAA GT

22

(2) INFORMATION FOR SEQ ID NO:1933

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

1436

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1933

CTTGAATTAG GGGCAAAGAT CG

22

(2) INFORMATION FOR SEQ ID NO:1934:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1934

ATGCGTTTTT ACCCAAAGAA GT

22

(2) INFORMATION FOR SEQ ID NO:1935:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1935

ATAACGCCAC TTCCTTATTG GT

22

(2) INFORMATION FOR SEQ ID NO:1936:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1936

CTTTGGGTAA AAACGCATC

19

(2) INFORMATION FOR SEQ ID NO:1937:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...20
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1937

CGATCTTTGA TCCTAATTCA

20

(2) INFORMATION FOR SEQ ID NO:1938:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1938

ATCAAGTTGC CTATGCTGA

19

(2) INFORMATION FOR SEQ ID NO:1939:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...22
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1939

TTGAACACTT TTGATTATGC GG

22

(2) INFORMATION FOR SEQ ID NO:1940:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...23
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1940

GGATTATGCG ATTGTTTTAC AAG

23

(2) INFORMATION FOR SEQ ID NO:1941:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

1439

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

- (ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...21
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1941

GTCTTTAGCA AAAATGGCGT C

21

(2) INFORMATION FOR SEQ ID NO:1942:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...21
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1942

AATGAGCGTA AGAGAGCCTT C

21

(2) INFORMATION FOR SEQ ID NO:1943:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
(ix) FEATURE:
 (A) NAME/KEY: misc_feature

(B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1943

CTTATGGGGG TATTGTCA

18

(2) INFORMATION FOR SEQ ID NO:1944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1944

AGCATGTGGG TATCCAGC

18

(2) INFORMATION FOR SEQ ID NO:1945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1945

AGGTTGTTGC CTAAAGACT

19

(2) INFORMATION FOR SEQ ID NO:1946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

1441

- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1946

CTGCCTCCAC CTTTGATC

18

(2) INFORMATION FOR SEQ ID NO:1947:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1947

ACCAATATCA ATTGGCACT

19

(2) INFORMATION FOR SEQ ID NO:1948:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1948

ACTTGGA AAA GCTCTGCA

18

1442

(2) INFORMATION FOR SEQ ID NO:1949:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...19
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1949

CTTGCTGTC ATATCTAGC

19

(2) INFORMATION FOR SEQ ID NO:1950:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...18
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1950

GTTGAAGTGT TGGTGCTA

18

(2) INFORMATION FOR SEQ ID NO:1951:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

1443

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1951

CAAGCAAGTG GTTTGGTTTT AG

22

(2) INFORMATION FOR SEQ ID NO:1952:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1952

TGGAAAGAGC AAATCATTGA AG

22

(2) INFORMATION FOR SEQ ID NO:1953:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1953

GCCCATATC AAAAAGCCCA T

21

(2) INFORMATION FOR SEQ ID NO:1954:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs

1444

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1954

CTAAAACCAA ACCACTTGCT TGTC

24

(2) INFORMATION FOR SEQ ID NO:1955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1955

GTAAAACGAC GGCCAG

16

(2) INFORMATION FOR SEQ ID NO:1956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1956

CAGGAAACAG CTATGAC

17

CLAIMS

1. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cell envelope polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO: 1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO: 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 217, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911, SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, SEQ ID NO: 215, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ

ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936,
 5 SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, SEQ ID NO: 210, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903, SEQ ID NO: 261,
 10 SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, SEQ ID NO: 966, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48,
 15 SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, SEQ ID NO: 977, SEQ ID NO: 978, SEQ ID NO: 994, SEQ ID NO: 163, SEQ ID NO: 256, SEQ ID NO: 287, SEQ ID NO: 184, SEQ ID NO: 45, SEQ ID NO: 136, SEQ ID NO: 214, SEQ ID NO: 16, SEQ ID NO: 192, SEQ ID NO: 373, SEQ ID NO: 892, SEQ ID NO: 239, SEQ ID NO: 34, SEQ ID NO: 340, SEQ ID NO: 41, SEQ ID NO: 332, SEQ ID NO: 134, and SEQ ID NO: 330.

2. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID
 25 NO: 1020, SEQ ID NO: 1021, SEQ ID NO: 1036, SEQ ID NO: 1050, SEQ ID NO: 1071, SEQ ID NO: 1101, SEQ ID NO: 1135, SEQ ID NO: 1276, SEQ ID NO: 1150, SEQ ID NO: 1187, SEQ ID NO: 1192, SEQ ID NO: 1361, SEQ ID NO: 1379, SEQ ID NO: 1399, SEQ ID NO: 1403, SEQ ID NO: 1400, SEQ ID NO: 1189, SEQ ID NO: 217, SEQ ID NO: 367, SEQ ID NO: 911, SEQ ID NO: 944, SEQ ID NO: 18, SEQ ID NO: 107, SEQ ID NO: 894, SEQ ID NO: 943, SEQ ID NO: 203, SEQ ID NO: 85, SEQ ID NO: 290, SEQ ID NO: 5, SEQ ID NO: 199, SEQ ID NO: 992, SEQ ID NO: 934, SEQ ID NO: 899, SEQ ID NO: 302, and SEQ ID NO: 215.

3. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1002, SEQ ID NO: 1213, SEQ ID NO: 1214, SEQ ID NO: 1215, SEQ ID NO: 1234, SEQ ID NO: 1236, SEQ ID NO: 1237, SEQ ID NO: 1224, SEQ ID NO: 1251, SEQ ID NO: 1262, SEQ ID NO: 1149, SEQ ID NO: 1220, SEQ ID NO: 1240, SEQ ID NO: 1164, SEQ
 40 ID NO: 1165, SEQ ID NO: 1404, SEQ ID NO: 1144, SEQ ID NO: 1182, SEQ ID NO:

1157, SEQ ID NO: 1160, SEQ ID NO: 1300, SEQ ID NO: 1321, SEQ ID NO: 1323, SEQ ID NO: 1329, SEQ ID NO: 1332, SEQ ID NO: 1345, SEQ ID NO: 1358, SEQ ID NO: 1375, SEQ ID NO: 1417, SEQ ID NO: 1283, SEQ ID NO: 1335, SEQ ID NO: 1368, SEQ ID NO: 1179, SEQ ID NO: 1255, SEQ ID NO: 1258, SEQ ID NO: 1044, SEQ ID NO: 1273, SEQ ID NO: 893, SEQ ID NO: 984, SEQ ID NO: 97, SEQ ID NO: 22, SEQ ID NO: 49, SEQ ID NO: 309, SEQ ID NO: 150, SEQ ID NO: 240, SEQ ID NO: 957, SEQ ID NO: 57, SEQ ID NO: 2, SEQ ID NO: 92, SEQ ID NO: 255, SEQ ID NO: 164, SEQ ID NO: 201, SEQ ID NO: 278, SEQ ID NO: 245, SEQ ID NO: 921, SEQ ID NO: 896, SEQ ID NO: 248, SEQ ID NO: 159, SEQ ID NO: 979, SEQ ID NO: 194, SEQ ID NO: 194, SEQ ID NO: 946, SEQ ID NO: 916, SEQ ID NO: 76, SEQ ID NO: 905, SEQ ID NO: 914, SEQ ID NO: 931, SEQ ID NO: 50, SEQ ID NO: 250, SEQ ID NO: 969, SEQ ID NO: 66, SEQ ID NO: 275, SEQ ID NO: 330, SEQ ID NO: 204, SEQ ID NO: 383, SEQ ID NO: 303, SEQ ID NO: 70, SEQ ID NO: 983, SEQ ID NO: 972, SEQ ID NO: 929, SEQ ID NO: 972, SEQ ID NO: 936, SEQ ID NO: 267, SEQ ID NO: 197, SEQ ID NO: 55, SEQ ID NO: 54, and SEQ ID NO: 210.

4. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1219, SEQ ID NO: 1274, SEQ ID NO: 1210, SEQ ID NO: 1422, SEQ ID NO: 1302, SEQ ID NO: 1308, SEQ ID NO: 1310, SEQ ID NO: 1331, SEQ ID NO: 1432, SEQ ID NO: 1052, SEQ ID NO: 1091, SEQ ID NO: 1421, SEQ ID NO: 1069, SEQ ID NO: 1005, SEQ ID NO: 1007, SEQ ID NO: 1166, SEQ ID NO: 1177, SEQ ID NO: 1193, SEQ ID NO: 1206, SEQ ID NO: 1207, SEQ ID NO: 1304, SEQ ID NO: 1305, SEQ ID NO: 1346, SEQ ID NO: 1348, SEQ ID NO: 1350, SEQ ID NO: 1032, SEQ ID NO: 1053, SEQ ID NO: 1081, SEQ ID NO: 1124, SEQ ID NO: 1382, SEQ ID NO: 1437, SEQ ID NO: 1263, SEQ ID NO: 90, SEQ ID NO: 15, SEQ ID NO: 913, SEQ ID NO: 227, SEQ ID NO: 79, SEQ ID NO: 191, SEQ ID NO: 238, SEQ ID NO: 274, SEQ ID NO: 27, SEQ ID NO: 258, SEQ ID NO: 295, SEQ ID NO: 10, SEQ ID NO: 160, SEQ ID NO: 225, SEQ ID NO: 964, SEQ ID NO: 166, SEQ ID NO: 56, SEQ ID NO: 980, SEQ ID NO: 903, SEQ ID NO: 261, SEQ ID NO: 71, SEQ ID NO: 955, SEQ ID NO: 361, SEQ ID NO: 58, SEQ ID NO: 114, SEQ ID NO: 940, SEQ ID NO: 960, SEQ ID NO: 144, SEQ ID NO: 362, SEQ ID NO: 40, SEQ ID NO: 285, SEQ ID NO: 11, SEQ ID NO: 161, SEQ ID NO: 974, SEQ ID NO: 111, SEQ ID NO: 316, SEQ ID NO: 257, SEQ ID NO: 78, and SEQ ID NO: 966.

5. The purified nucleic acid of claim 1, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1173, SEQ ID NO: 1405, SEQ ID NO: 1406, SEQ ID NO: 1410, SEQ ID NO: 1086, SEQ ID NO: 1322, SEQ ID NO: 1266, SEQ ID NO: 1282, SEQ ID NO: 1271, SEQ ID NO:

- 1208, SEQ ID NO: 1126, SEQ ID NO: 1270, SEQ ID NO: 1278, SEQ ID NO: 1419, SEQ ID NO: 1125, SEQ ID NO: 1181, SEQ ID NO: 1416, SEQ ID NO: 1096, SEQ ID NO: 1082, SEQ ID NO: 1146, SEQ ID NO: 1145, SEQ ID NO: 1108, SEQ ID NO: 1148, SEQ ID NO: 1337, SEQ ID NO: 1338, SEQ ID NO: 1424, SEQ ID NO: 1000, SEQ ID NO: 1027, SEQ ID NO: 1175, SEQ ID NO: 1330, SEQ ID NO: 352, SEQ ID NO: 981, SEQ ID NO: 158, SEQ ID NO: 989, SEQ ID NO: 963, SEQ ID NO: 48, SEQ ID NO: 68, SEQ ID NO: 135, SEQ ID NO: 910, SEQ ID NO: 236, SEQ ID NO: 241, SEQ ID NO: 949, SEQ ID NO: 945, SEQ ID NO: 207, and SEQ ID NO: 977.
6. A recombinant expression vector comprising the nucleic acid of claim 1 operably linked to a transcription regulatory element.
7. A cell comprising a recombinant expression vector of claim 6.
8. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 7 under conditions that permit expression of the polypeptide.
9. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* cytoplasmic polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217, SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 1003, SEQ ID NO: 1087, SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 1028, SEQ ID NO: 1037, SEQ ID NO: 1077, SEQ ID NO: 1115, SEQ ID NO: 1232, SEQ ID NO: 1241, SEQ ID NO: 1267, SEQ ID NO: 1163, SEQ ID NO:

1068, SEQ ID NO: 1025, SEQ ID NO: 1042, SEQ ID NO: 1046, SEQ ID NO: 1056, SEQ
ID NO: 1039, SEQ ID NO: 1072, SEQ ID NO: 1073, SEQ ID NO: 1092, SEQ ID NO:
1100, SEQ ID NO: 1102, SEQ ID NO: 1103, SEQ ID NO: 1104, SEQ ID NO: 1111, SEQ
ID NO: 1119, SEQ ID NO: 1136, SEQ ID NO: 1137, SEQ ID NO: 1140, SEQ ID NO:
5 1142, SEQ ID NO: 1233, SEQ ID NO: 1238, SEQ ID NO: 1243, SEQ ID NO: 1245, SEQ
ID NO: 1247, SEQ ID NO: 1249, SEQ ID NO: 1261, SEQ ID NO: 1269, SEQ ID NO:
1279, SEQ ID NO: 1284, SEQ ID NO: 1290, SEQ ID NO: 1297, SEQ ID NO: 1328, SEQ
ID NO: 1370, SEQ ID NO: 1372, SEQ ID NO: 1377, SEQ ID NO: 1383, SEQ ID NO:
1384, SEQ ID NO: 1385, SEQ ID NO: 1388, SEQ ID NO: 1401, SEQ ID NO: 1402, SEQ
10 ID NO: 1418, SEQ ID NO: 1420, SEQ ID NO: 1427, SEQ ID NO: 1070, SEQ ID NO:
1151, SEQ ID NO: 1176, SEQ ID NO: 999, SEQ ID NO: 1006, SEQ ID NO: 1012, SEQ
ID NO: 1018, SEQ ID NO: 1030, SEQ ID NO: 1033, SEQ ID NO: 1041, SEQ ID NO:
1049, SEQ ID NO: 1054, SEQ ID NO: 1057, SEQ ID NO: 1090, SEQ ID NO: 1097, SEQ
ID NO: 1129, SEQ ID NO: 1139, SEQ ID NO: 1143, SEQ ID NO: 1152, SEQ ID NO:
15 1153, SEQ ID NO: 1155, SEQ ID NO: 1161, SEQ ID NO: 1162, SEQ ID NO: 1169, SEQ
ID NO: 1170, SEQ ID NO: 1171, SEQ ID NO: 1180, SEQ ID NO: 1194, SEQ ID NO:
1195, SEQ ID NO: 1199, SEQ ID NO: 1200, SEQ ID NO: 1201, SEQ ID NO: 1202, SEQ
ID NO: 1205, SEQ ID NO: 1312, SEQ ID NO: 1336, SEQ ID NO: 1349, SEQ ID NO:
1355, SEQ ID NO: 1359, SEQ ID NO: 1413, SEQ ID NO: 1426, SEQ ID NO: 1430, SEQ
20 ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, SEQ ID NO: 230, SEQ ID NO: 269,
SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO:
110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID
NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID
NO: 326, SEQ ID NO: 272, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID
25 NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ
ID NO: 128, SEQ ID NO: 347, SEQ ID NO: 52, SEQ ID NO: 12, SEQ ID NO: 247, SEQ
ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID
NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, SEQ ID NO: 168, SEQ ID
NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, SEQ ID
30 NO: 4, SEQ ID NO: 197, SEQ ID NO: 313, SEQ ID NO: 119, SEQ ID NO: 188, SEQ ID
NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, SEQ ID NO: 376, SEQ
ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ
ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ
ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243,
35 SEQ ID NO: 19, SEQ ID NO: 9, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349,
SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, SEQ ID NO: 8,
SEQ ID NO: 887, SEQ ID NO: 350, SEQ ID NO: 987, SEQ ID NO: 63, SEQ ID NO: 249,
SEQ ID NO: 118, SEQ ID NO: 132, SEQ ID NO: 47, SEQ ID NO: 106, SEQ ID NO: 324,
SEQ ID NO: 155, SEQ ID NO: 121, SEQ ID NO: 153, SEQ ID NO: 87, SEQ ID NO: 986.

SEQ ID NO: 262, SEQ ID NO: 333, SEQ ID NO: 36, SEQ ID NO: 982, SEQ ID NO: 180, SEQ ID NO: 84, SEQ ID NO: 900, SEQ ID NO: 20, SEQ ID NO: 7, SEQ ID NO: 61, SEQ ID NO: 253, SEQ ID NO: 120, SEQ ID NO: 268, SEQ ID NO: 299, SEQ ID NO: 942, SEQ ID NO: 173, SEQ ID NO: 187, SEQ ID NO: 187, SEQ ID NO: 234, SEQ ID NO: 112, SEQ ID NO: 324, SEQ ID NO: 971, SEQ ID NO: 62, SEQ ID NO: 308, SEQ ID NO: 74, SEQ ID NO: 1, SEQ ID NO: 266, SEQ ID NO: 337, SEQ ID NO: 93, SEQ ID NO: 44, SEQ ID NO: 335, SEQ ID NO: 368, SEQ ID NO: 208, SEQ ID NO: 358, SEQ ID NO: 923, SEQ ID NO: 310, SEQ ID NO: 26, SEQ ID NO: 279, SEQ ID NO: 890, SEQ ID NO: 325, SEQ ID NO: 109, SEQ ID NO: 143, SEQ ID NO: 918, SEQ ID NO: 252, SEQ ID NO: 953, SEQ ID NO: 902, SEQ ID NO: 174, SEQ ID NO: 73, SEQ ID NO: 898, SEQ ID NO: 300, SEQ ID NO: 356, SEQ ID NO: 298, SEQ ID NO: 354, SEQ ID NO: 138, SEQ ID NO: 319, SEQ ID NO: 80, SEQ ID NO: 933, SEQ ID NO: 891, SEQ ID NO: 366, SEQ ID NO: 113, SEQ ID NO: 320, SEQ ID NO: 915, SEQ ID NO: 351, SEQ ID NO: 162, SEQ ID NO: 965, SEQ ID NO: 67, SEQ ID NO: 314, SEQ ID NO: 904, SEQ ID NO: 345, SEQ ID NO: 374, SEQ ID NO: 962, SEQ ID NO: 270, SEQ ID NO: 186, SEQ ID NO: 60, SEQ ID NO: 379, SEQ ID NO: 889, SEQ ID NO: 967, SEQ ID NO: 973, SEQ ID NO: 280, SEQ ID NO: 170, SEQ ID NO: 985, and SEQ ID NO: 932.

10. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1147, SEQ ID NO: 1288, SEQ ID NO: 1324, SEQ ID NO: 1363, SEQ ID NO: 882, SEQ ID NO: 382, SEQ ID NO: 130, and SEQ ID NO: 230.

11. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 997, SEQ ID NO: 1015, SEQ ID NO: 1084, SEQ ID NO: 1094, SEQ ID NO: 1099, SEQ ID NO: 1229, SEQ ID NO: 1250, SEQ ID NO: 1268, SEQ ID NO: 1293, SEQ ID NO: 1339, SEQ ID NO: 1408, SEQ ID NO: 1429, SEQ ID NO: 1434, SEQ ID NO: 1228, SEQ ID NO: 1031, SEQ ID NO: 1034, SEQ ID NO: 1008, SEQ ID NO: 269, SEQ ID NO: 312, SEQ ID NO: 211, SEQ ID NO: 959, SEQ ID NO: 938, SEQ ID NO: 110, SEQ ID NO: 244, SEQ ID NO: 328, SEQ ID NO: 235, SEQ ID NO: 315, SEQ ID NO: 296, SEQ ID NO: 976, SEQ ID NO: 321, SEQ ID NO: 43, SEQ ID NO: 281, SEQ ID NO: 326, and SEQ ID NO: 272.

12. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1061, SEQ ID NO: 1064, SEQ ID NO: 1191, SEQ ID NO: 1217,

SEQ ID NO: 1365, SEQ ID NO: 1394, SEQ ID NO: 1414, SEQ ID NO: 1415, SEQ ID NO: 1435, SEQ ID NO: 1058, SEQ ID NO: 1059, SEQ ID NO: 344, SEQ ID NO: 139, SEQ ID NO: 30, SEQ ID NO: 220, SEQ ID NO: 364, SEQ ID NO: 369, SEQ ID NO: 372, SEQ ID NO: 991, SEQ ID NO: 128, SEQ ID NO: 347, and SEQ ID NO: 52.

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13. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1080, SEQ ID NO: 1128, SEQ ID NO: 1133, SEQ ID NO: 1211, SEQ ID NO: 1252, SEQ ID NO: 1253, SEQ ID NO: 1286, SEQ ID NO: 1289, SEQ ID NO: 1291, SEQ ID NO: 1303, SEQ ID NO: 1396, SEQ ID NO: 996, SEQ ID NO: 12, SEQ ID NO: 247, SEQ ID NO: 64, SEQ ID NO: 101, SEQ ID NO: 338, SEQ ID NO: 83, SEQ ID NO: 46, SEQ ID NO: 348, SEQ ID NO: 223, SEQ ID NO: 39, SEQ ID NO: 232, and SEQ ID NO: 168.

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14. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1095, SEQ ID NO: 1156, SEQ ID NO: 1158, SEQ ID NO: 1159, SEQ ID NO: 1277, SEQ ID NO: 1038, SEQ ID NO: 65, SEQ ID NO: 952, SEQ ID NO: 341, SEQ ID NO: 69, SEQ ID NO: 924, and SEQ ID NO: 4.

15. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1257, SEQ ID NO: 1357, SEQ ID NO: 1436, SEQ ID NO: 197, SEQ ID NO: 313, and SEQ ID NO: 119.

16. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1047, SEQ ID NO: 1055, SEQ ID NO: 1141, SEQ ID NO: 1227, SEQ ID NO: 1327, SEQ ID NO: 1412, SEQ ID NO: 188, SEQ ID NO: 956, SEQ ID NO: 935, SEQ ID NO: 246, SEQ ID NO: 196, and SEQ ID NO: 376.

17. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1003, SEQ ID NO: 1087,

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SEQ ID NO: 1116, SEQ ID NO: 1130, SEQ ID NO: 1132, SEQ ID NO: 1185, SEQ ID NO: 1188, SEQ ID NO: 1198, SEQ ID NO: 1218, SEQ ID NO: 1244, SEQ ID NO: 1306, SEQ ID NO: 1325, SEQ ID NO: 1397, SEQ ID NO: 1398, SEQ ID NO: 1407, SEQ ID NO: 1433, SEQ ID NO: 172, SEQ ID NO: 25, SEQ ID NO: 126, SEQ ID NO: 951, SEQ ID NO: 147, SEQ ID NO: 895, SEQ ID NO: 14, SEQ ID NO: 154, SEQ ID NO: 277, SEQ ID NO: 363, SEQ ID NO: 342, SEQ ID NO: 378, SEQ ID NO: 130, SEQ ID NO: 198, SEQ ID NO: 243, SEQ ID NO: 19, and SEQ ID NO: 9.

18. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall biosynthesis encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1216, SEQ ID NO: 1239, SEQ ID NO: 1362, SEQ ID NO: 1017, SEQ ID NO: 1019, SEQ ID NO: 1360, SEQ ID NO: 149, SEQ ID NO: 167, SEQ ID NO: 349, SEQ ID NO: 209, SEQ ID NO: 990, SEQ ID NO: 185, SEQ ID NO: 883, and SEQ ID NO: 8.

19. The purified nucleic acid of claim 9, wherein said *H. pylori* cytoplasmic polypeptide is an *H. pylori* chaperone polypeptide or a fragment thereof encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1423, SEQ ID NO: 1425, SEQ ID NO: 1374, SEQ ID NO: 887, SEQ ID NO: 350, and SEQ ID NO: 987.

20. A recombinant expression vector comprising the nucleic acid of claim 9 operably linked to a transcription regulatory element.

21. A cell comprising a recombinant expression vector of claim 20.

22. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 21 under conditions that permit expression of the polypeptide.

23. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* secreted or periplasmic polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1004, SEQ ID NO: 1138, SEQ ID NO: 1067, SEQ ID NO: 1078, SEQ ID NO: 1314, SEQ ID NO: 1319, SEQ ID NO: 1378, SEQ ID NO: 1105, SEQ ID NO: 1114, SEQ ID NO: 1118, SEQ ID NO: 1120, SEQ ID NO: 1123, SEQ ID NO: 1127, SEQ ID NO: 1212, SEQ ID NO: 1223, SEQ ID NO: 1225, SEQ ID NO: 1246, SEQ ID NO: 1248, SEQ ID NO: 1259, SEQ ID NO: 1264, SEQ ID NO: 1265, SEQ ID NO: 1281, SEQ ID NO: 1285, SEQ ID NO: 1294, SEQ ID NO: 1298, SEQ ID NO: 1299, SEQ ID NO: 1315, SEQ ID NO: 1316, SEQ ID NO: 1317, SEQ ID NO: 1318, SEQ ID NO: 1344, SEQ ID NO: 1351, SEQ ID NO: 1353, SEQ ID NO: 1373, SEQ ID

NO: 1380, SEQ ID NO: 1387, SEQ ID NO: 1389, SEQ ID NO: 1393, SEQ ID NO: 1411,
 SEQ ID NO: 1428, SEQ ID NO: 1431, SEQ ID NO: 1439, SEQ ID NO: 1043, SEQ ID
 NO: 1183, SEQ ID NO: 1184, SEQ ID NO: 1196, SEQ ID NO: 1197, SEQ ID NO: 1203,
 SEQ ID NO: 995, SEQ ID NO: 998, SEQ ID NO: 1001, SEQ ID NO: 1022, SEQ ID NO:
 5 1023, SEQ ID NO: 1029, SEQ ID NO: 1040, SEQ ID NO: 1051, SEQ ID NO: 1062, SEQ
 ID NO: 1154, SEQ ID NO: 1320, SEQ ID NO: 1075, SEQ ID NO: 1106, SEQ ID NO:
 1109, SEQ ID NO: 1134, SEQ ID NO: 1221, SEQ ID NO: 1226, SEQ ID NO: 1235, SEQ
 ID NO: 1301, SEQ ID NO: 1311, SEQ ID NO: 1326, SEQ ID NO: 1341, SEQ ID NO:
 1354, SEQ ID NO: 1364, SEQ ID NO: 1366, SEQ ID NO: 1376, SEQ ID NO: 1391, SEQ
 10 ID NO: 1395, SEQ ID NO: 1445, SEQ ID NO: 1079, SEQ ID NO: 1186, SEQ ID NO:
 1010, SEQ ID NO: 1016, SEQ ID NO: 1172, SEQ ID NO: 1174, SEQ ID NO: 117, SEQ
 ID NO: 254, SEQ ID NO: 24, SEQ ID NO: 242, SEQ ID NO: 950, SEQ ID NO: 263, SEQ
 ID NO: 286, SEQ ID NO: 947, SEQ ID NO: 51, SEQ ID NO: 177, SEQ ID NO: 156, SEQ
 ID NO: 190, SEQ ID NO: 375, SEQ ID NO: 222, SEQ ID NO: 21, SEQ ID NO: 912, SEQ
 15 ID NO: 148, SEQ ID NO: 202, SEQ ID NO: 224, SEQ ID NO: 112, SEQ ID NO: 32, SEQ
 ID NO: 339, SEQ ID NO: 182, SEQ ID NO: 228, SEQ ID NO: 152, SEQ ID NO: 219,
 SEQ ID NO: 137, SEQ ID NO: 318, SEQ ID NO: 141, SEQ ID NO: 165, SEQ ID NO:
 334, SEQ ID NO: 13, SEQ ID NO: 297, SEQ ID NO: 35, SEQ ID NO: 216, SEQ ID NO:
 908, SEQ ID NO: 124, SEQ ID NO: 75, SEQ ID NO: 927, SEQ ID NO: 221, SEQ ID NO:
 20 178, SEQ ID NO: 169, SEQ ID NO: 293, SEQ ID NO: 289, SEQ ID NO: 926, SEQ ID
 NO: 948, SEQ ID NO: 115, SEQ ID NO: 251, SEQ ID NO: 345, SEQ ID NO: 17, SEQ ID
 NO: 920, SEQ ID NO: 95, SEQ ID NO: 86, SEQ ID NO: 360, SEQ ID NO: 271, SEQ ID
 NO: 970, SEQ ID NO: 288, SEQ ID NO: 282, SEQ ID NO: 98, SEQ ID NO: 29, SEQ ID
 NO: 317, SEQ ID NO: 343, SEQ ID NO: 291, SEQ ID NO: 108, SEQ ID NO: 377, SEQ
 25 ID NO: 305, SEQ ID NO: 305, SEQ ID NO: 100, SEQ ID NO: 988, SEQ ID NO: 212,
 SEQ ID NO: 884, SEQ ID NO: 37, SEQ ID NO: 968, SEQ ID NO: 975, SEQ ID NO: 237,
 SEQ ID NO: 335, SEQ ID NO: 260, SEQ ID NO: 370, SEQ ID NO: 91, SEQ ID NO: 276,
 SEQ ID NO: 311, SEQ ID NO: 173, SEQ ID NO: 102, SEQ ID NO: 304, SEQ ID NO:
 380, SEQ ID NO: 127, SEQ ID NO: 993, SEQ ID NO: 925, SEQ ID NO: 181, and SEQ ID
 30 NO: 171.

24. A recombinant expression vector comprising the nucleic acid of claim 23 operably linked to a transcription regulatory element.

35 25. A cell comprising a recombinant expression vector of claim 24.

26. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 25 under conditions that permit expression of the polypeptide.

27. An isolated nucleic acid comprising a nucleotide sequence encoding an *H. pylori* surface or membrane polypeptide or a fragment thereof, said nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ ID NO: 1209, SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO: 116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, SEQ ID NO: 365, SEQ ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, SEQ ID NO: 336, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, SEQ ID NO: 922, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, SEQ ID NO: 264, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, SEQ ID NO: 42, SEQ ID NO: 881, and SEQ ID NO: 885.

28. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1060, SEQ ID NO: 1110, SEQ ID NO: 1112, SEQ ID NO: 1230, SEQ ID NO: 1260, SEQ ID NO: 1280, SEQ ID NO: 1292, SEQ ID NO: 1296, SEQ ID NO: 1307, SEQ ID NO: 1442, SEQ ID NO: 1444, SEQ ID NO: 381, SEQ ID NO: 229, SEQ ID NO: 323, SEQ ID NO: 371, SEQ ID NO: 284, SEQ ID NO:

116, SEQ ID NO: 3, SEQ ID NO: 6, SEQ ID NO: 907, SEQ ID NO: 193, SEQ ID NO: 145, SEQ ID NO: 59, SEQ ID NO: 322, SEQ ID NO: 94, SEQ ID NO: 306, and SEQ ID NO: 881.

5 29. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1122, SEQ ID NO: 1254, SEQ ID NO: 1256, SEQ ID NO: 1272, SEQ ID NO: 1275, SEQ ID NO: 1309, SEQ ID NO: 1313, SEQ
10 ID NO: 1347, SEQ ID NO: 1352, SEQ ID NO: 1356, SEQ ID NO: 1438, SEQ ID NO: 1441, SEQ ID NO: 1009, SEQ ID NO: 1026, SEQ ID NO: 1048, SEQ ID NO: 1063, SEQ ID NO: 1190, SEQ ID NO: 939, SEQ ID NO: 205, SEQ ID NO: 123, SEQ ID NO: 906, SEQ ID NO: 928, SEQ ID NO: 346, SEQ ID NO: 129, SEQ ID NO: 307, SEQ ID NO: 133, SEQ ID NO: 131, SEQ ID NO: 886, SEQ ID NO: 179, SEQ ID NO: 104, SEQ ID
15 NO: 213, SEQ ID NO: 359, SEQ ID NO: 140, SEQ ID NO: 146, SEQ ID NO: 327, and SEQ ID NO: 365.

 30. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1083, SEQ ID NO: 1113, SEQ ID NO: 1222, SEQ ID NO: 1295, SEQ ID NO: 1343, SEQ ID NO: 1392, SEQ ID NO: 1443, SEQ
20 ID NO: 33, SEQ ID NO: 331, SEQ ID NO: 175, SEQ ID NO: 200, SEQ ID NO: 292, SEQ ID NO: 23, and SEQ ID NO: 336.

25 31. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1085, SEQ ID NO: 1093, SEQ ID NO: 1117, SEQ ID NO: 1121, SEQ ID NO: 1131, SEQ ID NO: 1287, SEQ ID NO: 1440, SEQ
30 ID NO: 1209, SEQ ID NO: 301, SEQ ID NO: 28, SEQ ID NO: 941, SEQ ID NO: 103, SEQ ID NO: 231, SEQ ID NO: 176, SEQ ID NO: 31, SEQ ID NO: 917, SEQ ID NO: 151, and SEQ ID NO: 922.

35 32. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1342, SEQ ID NO: 1381, SEQ ID NO: 1390, SEQ ID NO: 1409, SEQ ID NO: 1035, SEQ ID NO: 265, SEQ ID NO: 142, SEQ ID
40 NO: 259, SEQ ID NO: 122, SEQ ID NO: 206, and SEQ ID NO: 885.

33. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions encoded by the nucleic acid selected
5 from the group consisting of SEQ ID NO: 1014, SEQ ID NO: 1088, SEQ ID NO: 1242, SEQ ID NO: 1178, SEQ ID NO: 96, SEQ ID NO: 353, SEQ ID NO: 38, SEQ ID NO: 89, SEQ ID NO: 77, SEQ ID NO: 954, and SEQ ID NO: 264.

34. The purified nucleic acid of claim 27, wherein said *H. pylori* surface or
10 membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions encoded by the nucleic acid selected from the group consisting of SEQ ID NO: 1089, SEQ ID NO: 1340, SEQ ID NO: 1074, SEQ ID NO: 1107, SEQ ID NO: 1204, SEQ ID NO: 1066, SEQ ID NO: 937, SEQ ID NO: 226, SEQ ID NO: 283, SEQ ID NO: 88, SEQ ID NO: 125, SEQ ID NO: 183, SEQ
15 ID NO: 195, SEQ ID NO: 81, SEQ ID NO: 901, SEQ ID NO: 82, and SEQ ID NO: 42.

35. A recombinant expression vector comprising the nucleic acid of claim 27 operably linked to a transcription regulatory element.

20 36. A cell comprising a recombinant expression vector of claim 35.

37. A method for producing an *H. pylori* polypeptide comprising culturing a cell of claim 36 under conditions that permit expression of the polypeptide.

25 38. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 1.

39. A vaccine composition of claim 38, further comprising a pharmaceutically acceptable carrier.
30

40. A vaccine composition of claim 39, wherein the pharmaceutically acceptable carrier is an adjuvant.

41. A method of treating a subject for *H. pylori* infection comprising
35 administering to a subject a vaccine composition of claim 38, such that treatment of *H. pylori* infection occurs.

42. A method of claim 41, wherein the treatment is a prophylactic treatment.
40

43. A method of claim 41, wherein the treatment is a therapeutic treatment.
44. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 9.
- 5 45. A vaccine composition of claim 44, further comprising a pharmaceutically acceptable carrier.
- 10 46. A vaccine composition of claim 45, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 15 47. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 44, such that treatment of *H. pylori* infection occurs.
- 20 48. A method of claim 47, wherein the treatment is a prophylactic treatment.
49. A method of claim 47, wherein the treatment is a therapeutic treatment.
50. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of a nucleic acid of claim 23.
- 25 51. A vaccine composition of claim 50, further comprising a pharmaceutically acceptable carrier.
52. A vaccine composition of claim 51, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 30 53. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 50, such that treatment of *H. pylori* infection occurs.
- 35 54. A method of claim 53, wherein the treatment is a prophylactic treatment.
55. A method of claim 53, wherein the treatment is a therapeutic treatment.

56. A purified *H. pylori* cell envelope polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611, SEQ ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO: 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO: 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO: 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO: 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO: 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO: 1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, SEQ ID NO: 658, SEQ ID NO: 463, SEQ ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782, SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO: 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684, SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO: 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID NO: 737, SEQ ID NO:

809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788, SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO: 448, SEQ ID NO: 653, SEQ ID NO: 495, SEQ ID NO: 400, SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO: 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ ID NO: 451, SEQ ID NO: 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469, SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO: 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, SEQ ID NO: 765, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, SEQ ID NO: 812, SEQ ID NO: 820, SEQ ID NO: 880, SEQ ID NO: 590, SEQ ID NO: 713, SEQ ID NO: 750, SEQ ID NO: 613, SEQ ID NO: 437, SEQ ID NO: 556, SEQ ID NO: 657, SEQ ID NO: 402, SEQ ID NO: 623, SEQ ID NO: 862, SEQ ID NO: 449, SEQ ID NO: 690, SEQ ID NO: 424, SEQ ID NO: 821, SEQ ID NO: 432, SEQ ID NO: 811, SEQ ID NO: 554, and SEQ ID NO: 809.

20

57. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* flagella-associated polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1471, SEQ ID NO: 1472, SEQ ID NO: 1487, SEQ ID NO: 1501, SEQ ID NO: 1522, SEQ ID NO: 1552, SEQ ID NO: 1586, SEQ ID NO: 1727, SEQ ID NO: 1601, SEQ ID NO: 1638, SEQ ID NO: 1643, SEQ ID NO: 1812, SEQ ID NO: 1830, SEQ ID NO: 1850, SEQ ID NO: 1854, SEQ ID NO: 1851, SEQ ID NO: 1640, SEQ ID NO: 660, SEQ ID NO: 660, SEQ ID NO: 855, SEQ ID NO: 534, SEQ ID NO: 675, SEQ ID NO: 404, SEQ ID NO: 518, SEQ ID NO: 464, SEQ ID NO: 672, SEQ ID NO: 640, SEQ ID NO: 490, SEQ ID NO: 755, SEQ ID NO: 389, SEQ ID NO: 635, SEQ ID NO: 877, SEQ ID NO: 637, SEQ ID NO: 477, SEQ ID NO: 772, and SEQ ID NO: 658.

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58. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope polypeptide or a fragment thereof is an *H. pylori* inner membrane polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1453, SEQ ID NO: 1664, SEQ ID NO: 1665, SEQ ID NO: 1666, SEQ ID NO: 1685, SEQ ID NO: 1687, SEQ ID NO: 1688, SEQ ID NO: 1675, SEQ ID NO: 1702, SEQ ID NO: 1713, SEQ ID NO: 1600, SEQ ID NO: 1671, SEQ ID NO: 1691, SEQ ID NO: 1615, SEQ ID NO: 1616, SEQ ID NO: 1855, SEQ ID NO: 1595, SEQ ID NO: 1633, SEQ ID NO: 1608, SEQ ID NO: 1611. SEQ

35

ID NO: 1751, SEQ ID NO: 1772, SEQ ID NO: 1774, SEQ ID NO: 1780, SEQ ID NO:
 1783, SEQ ID NO: 1796, SEQ ID NO: 1809, SEQ ID NO: 1826, SEQ ID NO: 1868, SEQ
 ID NO: 1734, SEQ ID NO: 1786, SEQ ID NO: 1819, SEQ ID NO: 1630, SEQ ID NO:
 1706, SEQ ID NO: 1709, SEQ ID NO: 1495, SEQ ID NO: 1724, SEQ ID NO: 463, SEQ
 5 ID NO: 852, SEQ ID NO: 503, SEQ ID NO: 411, SEQ ID NO: 441, SEQ ID NO: 782,
 SEQ ID NO: 575, SEQ ID NO: 691, SEQ ID NO: 724, SEQ ID NO: 452, SEQ ID NO:
 386, SEQ ID NO: 497, SEQ ID NO: 712, SEQ ID NO: 591, SEQ ID NO: 638, SEQ ID
 NO: 740, SEQ ID NO: 697, SEQ ID NO: 569, SEQ ID NO: 470, SEQ ID NO: 700, SEQ
 ID NO: 586, SEQ ID NO: 823, SEQ ID NO: 627, SEQ ID NO: 627, SEQ ID NO: 684,
 10 SEQ ID NO: 551, SEQ ID NO: 478, SEQ ID NO: 508, SEQ ID NO: 545, SEQ ID NO:
 628, SEQ ID NO: 443, SEQ ID NO: 702, SEQ ID NO: 776, SEQ ID NO: 461, SEQ ID
 NO: 737, SEQ ID NO: 809, SEQ ID NO: 642, SEQ ID NO: 879, SEQ ID NO: 773, SEQ
 ID NO: 468, SEQ ID NO: 842, SEQ ID NO: 788, SEQ ID NO: 624, SEQ ID NO: 788,
 SEQ ID NO: 644, SEQ ID NO: 727, SEQ ID NO: 631, SEQ ID NO: 450, SEQ ID NO:
 15 448, and SEQ ID NO: 653.

59. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope
 polypeptide or a fragment thereof is an *H. pylori* transporter polypeptide or a fragment
 thereof selected from the group consisting of SEQ ID NO: 1670, SEQ ID NO: 1725, SEQ
 20 ID NO: 1661, SEQ ID NO: 1873, SEQ ID NO: 1753, SEQ ID NO: 1759, SEQ ID NO:
 1761, SEQ ID NO: 1782, SEQ ID NO: 1883, SEQ ID NO: 1503, SEQ ID NO: 1542, SEQ
 ID NO: 1872, SEQ ID NO: 1520, SEQ ID NO: 1456, SEQ ID NO: 1458, SEQ ID NO:
 1617, SEQ ID NO: 1628, SEQ ID NO: 1644, SEQ ID NO: 1657, SEQ ID NO: 1658, SEQ
 ID NO: 1755, SEQ ID NO: 1756, SEQ ID NO: 1797, SEQ ID NO: 1799, SEQ ID NO:
 25 1801, SEQ ID NO: 1483, SEQ ID NO: 1504, SEQ ID NO: 1532, SEQ ID NO: 1575, SEQ
 ID NO: 1833, SEQ ID NO: 1888, SEQ ID NO: 1714, SEQ ID NO: 495, SEQ ID NO: 400,
 SEQ ID NO: 541, SEQ ID NO: 673, SEQ ID NO: 482, SEQ ID NO: 622, SEQ ID NO:
 689, SEQ ID NO: 736, SEQ ID NO: 417, SEQ ID NO: 716, SEQ ID NO: 762, SEQ ID
 NO: 395, SEQ ID NO: 587, SEQ ID NO: 669, SEQ ID NO: 758, SEQ ID NO: 593, SEQ
 30 ID NO: 451, SEQ ID NO: 827, SEQ ID NO: 502, SEQ ID NO: 719, SEQ ID NO: 469,
 SEQ ID NO: 715, SEQ ID NO: 847, SEQ ID NO: 453, SEQ ID NO: 527, SEQ ID NO:
 652, SEQ ID NO: 745, SEQ ID NO: 567, SEQ ID NO: 848, SEQ ID NO: 430, SEQ ID
 NO: 748, SEQ ID NO: 396, SEQ ID NO: 588, SEQ ID NO: 795, SEQ ID NO: 523, SEQ
 ID NO: 791, SEQ ID NO: 714, SEQ ID NO: 481, and SEQ ID NO: 765.

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60. The purified polypeptide of claim 56, wherein said *H. pylori* cell envelope
 polypeptide or a fragment thereof is an *H. pylori* outer membrane polypeptide or a fragment
 thereof selected from the group consisting of SEQ ID NO: 1624, SEQ ID NO: 1856, SEQ
 ID NO: 1857, SEQ ID NO: 1861, SEQ ID NO: 1537, SEQ ID NO: 1773, SEQ ID NO:

1717, SEQ ID NO: 1733, SEQ ID NO: 1722, SEQ ID NO: 1659, SEQ ID NO: 1577, SEQ ID NO: 1721, SEQ ID NO: 1729, SEQ ID NO: 1870, SEQ ID NO: 1576, SEQ ID NO: 1632, SEQ ID NO: 1867, SEQ ID NO: 1547, SEQ ID NO: 1533, SEQ ID NO: 1597, SEQ ID NO: 1596, SEQ ID NO: 1559, SEQ ID NO: 1599, SEQ ID NO: 1788, SEQ ID NO: 1789, SEQ ID NO: 1875, SEQ ID NO: 1451, SEQ ID NO: 1478, SEQ ID NO: 1626, SEQ ID NO: 1781, SEQ ID NO: 837, SEQ ID NO: 833, SEQ ID NO: 585, SEQ ID NO: 865, SEQ ID NO: 764, SEQ ID NO: 440, SEQ ID NO: 465, SEQ ID NO: 555, SEQ ID NO: 526, SEQ ID NO: 687, SEQ ID NO: 692, SEQ ID NO: 693, SEQ ID NO: 677, SEQ ID NO: 649, and SEQ ID NO: 812.

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61. A purified *H. pylori* cytoplasmic polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 1479, SEQ ID NO: 1488, SEQ ID NO: 1528, SEQ ID NO: 1566, SEQ ID NO: 1683, SEQ ID NO: 1692, SEQ ID NO: 1718, SEQ ID NO: 1614, SEQ ID NO: 1519, SEQ ID NO: 1476, SEQ ID NO: 1493, SEQ ID NO: 1497, SEQ ID NO: 1507, SEQ ID NO: 1490, SEQ ID NO: 1523, SEQ ID NO: 1524, SEQ ID NO: 1543, SEQ ID NO: 1551, SEQ ID NO: 1553, SEQ ID NO: 1554, SEQ ID NO: 1555, SEQ ID NO: 1562, SEQ ID NO: 1570, SEQ ID NO: 1587, SEQ ID NO: 1588, SEQ ID NO: 1591, SEQ ID NO: 1593, SEQ ID NO: 1684, SEQ ID NO: 1689, SEQ ID NO: 1694, SEQ ID NO: 1696, SEQ ID NO: 1698, SEQ ID NO: 1700, SEQ ID NO: 1712, SEQ ID NO: 1720, SEQ ID NO: 1730, SEQ ID NO: 1735, SEQ ID NO: 1741, SEQ ID NO: 1748, SEQ

ID NO: 1779, SEQ ID NO: 1821, SEQ ID NO: 1823, SEQ ID NO: 1828, SEQ ID NO:
1834, SEQ ID NO: 1835, SEQ ID NO: 1836, SEQ ID NO: 1839, SEQ ID NO: 1852, SEQ
ID NO: 1853, SEQ ID NO: 1869, SEQ ID NO: 1871, SEQ ID NO: 1878, SEQ ID NO:
1521, SEQ ID NO: 1602, SEQ ID NO: 1627, SEQ ID NO: 1450, SEQ ID NO: 1457, SEQ
5 ID NO: 1463, SEQ ID NO: 1469, SEQ ID NO: 1481, SEQ ID NO: 1484, SEQ ID NO:
1492, SEQ ID NO: 1500, SEQ ID NO: 1505, SEQ ID NO: 1508, SEQ ID NO: 1541, SEQ
ID NO: 1548, SEQ ID NO: 1580, SEQ ID NO: 1590, SEQ ID NO: 1594, SEQ ID NO:
1603, SEQ ID NO: 1604, SEQ ID NO: 1606, SEQ ID NO: 1612, SEQ ID NO: 1613, SEQ
ID NO: 1620, SEQ ID NO: 1621, SEQ ID NO: 1622, SEQ ID NO: 1631, SEQ ID NO:
10 1645, SEQ ID NO: 1646, SEQ ID NO: 1650, SEQ ID NO: 1651, SEQ ID NO: 1652, SEQ
ID NO: 1653, SEQ ID NO: 1656, SEQ ID NO: 1763, SEQ ID NO: 1787, SEQ ID NO:
1800, SEQ ID NO: 1806, SEQ ID NO: 1810, SEQ ID NO: 1864, SEQ ID NO: 1877, SEQ
ID NO: 1881, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678,
SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO:
15 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID
NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ
ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733, SEQ ID NO: 826, SEQ ID NO: 562,
SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO:
861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, SEQ ID NO: 446, SEQ ID
20 NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ
ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429,
SEQ ID NO: 680, SEQ ID NO: 597, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO:
822, SEQ ID NO: 466, SEQ ID NO: 584, SEQ ID NO: 388, SEQ ID NO: 631, SEQ ID
NO: 787, SEQ ID NO: 532, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ
25 ID NO: 698, SEQ ID NO: 630, SEQ ID NO: 869, SEQ ID NO: 601, SEQ ID NO: 415,
SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO:
399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID
NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ
ID NO: 394, SEQ ID NO: 761, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832,
30 SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, SEQ ID NO:
393, SEQ ID NO: 413, SEQ ID NO: 835, SEQ ID NO: 863, SEQ ID NO: 458, SEQ ID
NO: 701, SEQ ID NO: 531, SEQ ID NO: 550, SEQ ID NO: 439, SEQ ID NO: 516, SEQ
ID NO: 802, SEQ ID NO: 581, SEQ ID NO: 535, SEQ ID NO: 578, SEQ ID NO: 492,
SEQ ID NO: 858, SEQ ID NO: 720, SEQ ID NO: 813, SEQ ID NO: 426, SEQ ID NO:
35 834, SEQ ID NO: 609, SEQ ID NO: 489, SEQ ID NO: 480, SEQ ID NO: 406, SEQ ID
NO: 392, SEQ ID NO: 456, SEQ ID NO: 707, SEQ ID NO: 533, SEQ ID NO: 728, SEQ
ID NO: 769, SEQ ID NO: 671, SEQ ID NO: 602, SEQ ID NO: 618, SEQ ID NO: 618,
SEQ ID NO: 682, SEQ ID NO: 524, SEQ ID NO: 802, SEQ ID NO: 785, SEQ ID NO:
457, SEQ ID NO: 781, SEQ ID NO: 473, SEQ ID NO: 384, SEQ ID NO: 726, SEQ ID

NO: 817, SEQ ID NO: 498, SEQ ID NO: 436, SEQ ID NO: 815, SEQ ID NO: 856, SEQ ID NO: 650, SEQ ID NO: 844, SEQ ID NO: 580, SEQ ID NO: 783, SEQ ID NO: 416, SEQ ID NO: 741, SEQ ID NO: 442, SEQ ID NO: 803, SEQ ID NO: 520, SEQ ID NO: 566, SEQ ID NO: 557, SEQ ID NO: 706, SEQ ID NO: 710, SEQ ID NO: 487, SEQ ID NO: 603, SEQ ID NO: 472, SEQ ID NO: 476, SEQ ID NO: 770, SEQ ID NO: 841, SEQ ID NO: 768, SEQ ID NO: 839, SEQ ID NO: 560, SEQ ID NO: 796, SEQ ID NO: 483, SEQ ID NO: 634, SEQ ID NO: 445, SEQ ID NO: 853, SEQ ID NO: 525, SEQ ID NO: 798, SEQ ID NO: 549, SEQ ID NO: 836, SEQ ID NO: 589, SEQ ID NO: 760, SEQ ID NO: 462, SEQ ID NO: 789, SEQ ID NO: 507, SEQ ID NO: 828, SEQ ID NO: 866, SEQ ID NO: 754, SEQ ID NO: 730, SEQ ID NO: 617, SEQ ID NO: 455, SEQ ID NO: 873, SEQ ID NO: 435, SEQ ID NO: 766, SEQ ID NO: 793, SEQ ID NO: 742, SEQ ID NO: 599, SEQ ID NO: 854, and SEQ ID NO: 632.

62. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in energy conversion selected from the group consisting of SEQ ID NO: 1598, SEQ ID NO: 1739, SEQ ID NO: 1775, SEQ ID NO: 1814, SEQ ID NO: 390, SEQ ID NO: 876, SEQ ID NO: 547, SEQ ID NO: 678.

63. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in amino acid metabolism selected from the group consisting of SEQ ID NO: 1448, SEQ ID NO: 1466, SEQ ID NO: 1535, SEQ ID NO: 1545, SEQ ID NO: 1550, SEQ ID NO: 1680, SEQ ID NO: 1701, SEQ ID NO: 1719, SEQ ID NO: 1744, SEQ ID NO: 1790, SEQ ID NO: 1859, SEQ ID NO: 1880, SEQ ID NO: 1885, SEQ ID NO: 1679, SEQ ID NO: 1482, SEQ ID NO: 1485, SEQ ID NO: 1459, SEQ ID NO: 729, SEQ ID NO: 786, SEQ ID NO: 654, SEQ ID NO: 734, SEQ ID NO: 646, SEQ ID NO: 522, SEQ ID NO: 696, SEQ ID NO: 807, SEQ ID NO: 683, SEQ ID NO: 790, SEQ ID NO: 763, SEQ ID NO: 806, SEQ ID NO: 799, SEQ ID NO: 434, SEQ ID NO: 743, SEQ ID NO: 804, SEQ ID NO: 733.

64. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in nucleotide metabolism selected from the group consisting of SEQ ID NO: 1512, SEQ ID NO: 1515, SEQ ID NO: 1642, SEQ ID NO: 1668, SEQ ID NO: 1816, SEQ ID NO: 1845, SEQ ID NO: 1865, SEQ ID NO: 1866, SEQ ID NO: 1886, SEQ ID NO: 1509, SEQ ID NO: 1510, SEQ ID NO: 826, SEQ ID NO: 562, SEQ ID NO: 420, SEQ ID NO: 664, SEQ ID NO: 850, SEQ ID NO: 857, SEQ ID NO: 861, SEQ ID NO: 872, SEQ ID NO: 544, SEQ ID NO: 830, and SEQ ID NO: 446.

65. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in carbohydrate metabolism selected from the group consisting of SEQ ID NO: 1531, SEQ ID NO: 1579, SEQ ID NO: 1584, SEQ ID NO: 1662, SEQ ID NO: 1703, SEQ ID NO: 1704, SEQ ID NO: 1737, SEQ ID NO: 1740, SEQ ID NO: 1742, SEQ ID NO: 1754, SEQ ID NO: 1847, SEQ ID NO: 1447, SEQ ID NO: 397, SEQ ID NO: 699, SEQ ID NO: 459, SEQ ID NO: 509, SEQ ID NO: 818, SEQ ID NO: 488, SEQ ID NO: 438, SEQ ID NO: 831, SEQ ID NO: 667, SEQ ID NO: 429, SEQ ID NO: 680, and SEQ ID NO: 597.

66. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in cofactor metabolism selected from the group consisting of SEQ ID NO: 1546, SEQ ID NO: 1607, SEQ ID NO: 1609, SEQ ID NO: 1610, SEQ ID NO: 1728, SEQ ID NO: 1489, SEQ ID NO: 460, SEQ ID NO: 709, SEQ ID NO: 822, SEQ ID NO: 466, SEQ ID NO: 584, and SEQ ID NO: 388.

67. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in lipid metabolism selected from the group consisting of SEQ ID NO: 1708, SEQ ID NO: 1808, SEQ ID NO: 1887, SEQ ID NO: 631, SEQ ID NO: 787, and SEQ ID NO: 532.

68. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in mRNA translation and ribosome biogenesis selected from the group consisting of SEQ ID NO: 1498, SEQ ID NO: 1506, SEQ ID NO: 1592, SEQ ID NO: 1678, SEQ ID NO: 1778, SEQ ID NO: 1863, SEQ ID NO: 619, SEQ ID NO: 723, SEQ ID NO: 641, SEQ ID NO: 698, SEQ ID NO: 630, and SEQ ID NO: 869.

69. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in genome replication, transcription, recombination and repair selected from the group consisting of SEQ ID NO: 1454, SEQ ID NO: 1538, SEQ ID NO: 1567, SEQ ID NO: 1581, SEQ ID NO: 1583, SEQ ID NO: 1636, SEQ ID NO: 1639, SEQ ID NO: 1649, SEQ ID NO: 1669, SEQ ID NO: 1695, SEQ ID NO: 1757, SEQ ID NO: 1776, SEQ ID NO: 1848, SEQ ID NO: 1849, SEQ ID NO: 1858, SEQ ID NO: 1884, SEQ ID NO: 601, SEQ ID NO: 415, SEQ ID NO: 542, SEQ ID NO: 704, SEQ ID NO: 572, SEQ ID NO: 467, SEQ ID NO: 399, SEQ ID NO: 579, SEQ ID NO: 739, SEQ ID NO: 849, SEQ ID NO: 824, SEQ ID NO: 871, SEQ ID NO: 547, SEQ ID NO: 633, SEQ ID NO: 695, SEQ ID NO: 405, SEQ ID NO: 394, and SEQ ID NO: 761.

70. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof involved in outer membrane or cell wall biosynthesis selected from the group consisting of
5 SEQ ID NO: 1667, SEQ ID NO: 1690, SEQ ID NO: 1813, SEQ ID NO: 1468, SEQ ID NO: 1470, SEQ ID NO: 1811, SEQ ID NO: 574, SEQ ID NO: 596, SEQ ID NO: 832, SEQ ID NO: 651, SEQ ID NO: 867, SEQ ID NO: 614, SEQ ID NO: 401, and SEQ ID NO: 393.

71. The purified polypeptide of claim 61, wherein said *H. pylori* cytoplasmic
10 polypeptide or a fragment thereof is an *H. pylori* chaperone polypeptide or a fragment thereof selected from the group consisting of SEQ ID NO: 1874, SEQ ID NO: 1876, SEQ ID NO: 1825, SEQ ID NO: 413, SEQ ID NO: 835, and SEQ ID NO: 863.

72. A purified *H. pylori* secreted or periplasmic polypeptide or a fragment
15 thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1455, SEQ ID NO: 1589, SEQ ID NO: 1518, SEQ ID NO: 1529, SEQ ID NO: 1765, SEQ ID NO: 1770, SEQ ID NO: 1829, SEQ ID NO: 1556, SEQ ID NO: 1565, SEQ ID NO: 1569, SEQ ID NO: 1571, SEQ ID NO: 1574, SEQ ID NO: 1578, SEQ ID NO: 1663, SEQ ID NO: 1674, SEQ ID NO: 1676, SEQ ID NO: 1697, SEQ ID NO: 1699, SEQ ID NO:
20 1710, SEQ ID NO: 1715, SEQ ID NO: 1716, SEQ ID NO: 1732, SEQ ID NO: 1736, SEQ ID NO: 1745, SEQ ID NO: 1749, SEQ ID NO: 1750, SEQ ID NO: 1766, SEQ ID NO: 1767, SEQ ID NO: 1768, SEQ ID NO: 1769, SEQ ID NO: 1795, SEQ ID NO: 1802, SEQ ID NO: 1804, SEQ ID NO: 1824, SEQ ID NO: 1831, SEQ ID NO: 1838, SEQ ID NO: 1840, SEQ ID NO: 1844, SEQ ID NO: 1862, SEQ ID NO: 1879, SEQ ID NO: 1882, SEQ
25 ID NO: 1890, SEQ ID NO: 1494, SEQ ID NO: 1634, SEQ ID NO: 1635, SEQ ID NO: 1647, SEQ ID NO: 1648, SEQ ID NO: 1654, SEQ ID NO: 1446, SEQ ID NO: 1449, SEQ ID NO: 1452, SEQ ID NO: 1473, SEQ ID NO: 1474, SEQ ID NO: 1480, SEQ ID NO: 1491, SEQ ID NO: 1502, SEQ ID NO: 1513, SEQ ID NO: 1605, SEQ ID NO: 1771, SEQ ID NO: 1526, SEQ ID NO: 1557, SEQ ID NO: 1560, SEQ ID NO: 1585, SEQ ID NO:
30 1672, SEQ ID NO: 1677, SEQ ID NO: 1686, SEQ ID NO: 1752, SEQ ID NO: 1762, SEQ ID NO: 1777, SEQ ID NO: 1792, SEQ ID NO: 1805, SEQ ID NO: 1815, SEQ ID NO: 1817, SEQ ID NO: 1827, SEQ ID NO: 1842, SEQ ID NO: 1846, SEQ ID NO: 1896, SEQ ID NO: 1530, SEQ ID NO: 1637, SEQ ID NO: 1461, SEQ ID NO: 1467, SEQ ID NO: 1623, SEQ ID NO: 1625, SEQ ID NO: 530, SEQ ID NO: 708, SEQ ID NO: 414, SEQ ID
35 NO: 694, SEQ ID NO: 703, SEQ ID NO: 721, SEQ ID NO: 749, SEQ ID NO: 685, SEQ ID NO: 444, SEQ ID NO: 606, SEQ ID NO: 582, SEQ ID NO: 621, SEQ ID NO: 868, SEQ ID NO: 666, SEQ ID NO: 408, SEQ ID NO: 538, SEQ ID NO: 573, SEQ ID NO: 639, SEQ ID NO: 668, SEQ ID NO: 524, SEQ ID NO: 422, SEQ ID NO: 819, SEQ ID NO: 611, SEQ ID NO: 674, SEQ ID NO: 577, SEQ ID NO: 663, SEQ ID NO: 558, SEQ

ID NO: 794, SEQ ID NO: 564, SEQ ID NO: 592, SEQ ID NO: 814, SEQ ID NO: 398, SEQ ID NO: 767, SEQ ID NO: 425, SEQ ID NO: 659, SEQ ID NO: 517, SEQ ID NO: 539, SEQ ID NO: 475, SEQ ID NO: 615, SEQ ID NO: 665, SEQ ID NO: 607, SEQ ID NO: 598, SEQ ID NO: 759, SEQ ID NO: 752, SEQ ID NO: 595, SEQ ID NO: 686, SEQ ID NO: 528, SEQ ID NO: 705, SEQ ID NO: 828, SEQ ID NO: 403, SEQ ID NO: 561, SEQ ID NO: 500, SEQ ID NO: 491, SEQ ID NO: 846, SEQ ID NO: 732, SEQ ID NO: 778, SEQ ID NO: 751, SEQ ID NO: 744, SEQ ID NO: 504, SEQ ID NO: 419, SEQ ID NO: 792, SEQ ID NO: 825, SEQ ID NO: 756, SEQ ID NO: 519, SEQ ID NO: 870, SEQ ID NO: 777, SEQ ID NO: 808, SEQ ID NO: 506, SEQ ID NO: 864, SEQ ID NO: 655, SEQ ID NO: 407, SEQ ID NO: 427, SEQ ID NO: 774, SEQ ID NO: 797, SEQ ID NO: 688, SEQ ID NO: 815, SEQ ID NO: 718, SEQ ID NO: 859, SEQ ID NO: 775, SEQ ID NO: 874, SEQ ID NO: 543, SEQ ID NO: 878, SEQ ID NO: 594, SEQ ID NO: 610, and SEQ ID NO: 600.

73. A purified *H. pylori* surface or membrane polypeptide or a fragment thereof, wherein said polypeptide is selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, SEQ ID NO: 851, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, SEQ ID NO: 816, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID

NO: 576, SEQ ID NO: 571, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, SEQ ID NO: 722, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, SEQ ID NO: 433, SEQ ID NO: 385, and SEQ ID NO: 409.

74. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least one membrane spanning region selected from the group consisting of SEQ ID NO: 1511, SEQ ID NO: 1561, SEQ ID NO: 1563, SEQ ID NO: 1681, SEQ ID NO: 1711, SEQ ID NO: 1731, SEQ ID NO: 1743, SEQ ID NO: 1747, SEQ ID NO: 1758, SEQ ID NO: 1893, SEQ ID NO: 1895, SEQ ID NO: 875, SEQ ID NO: 676, SEQ ID NO: 801, SEQ ID NO: 860, SEQ ID NO: 747, SEQ ID NO: 529, SEQ ID NO: 387, SEQ ID NO: 391, SEQ ID NO: 515, SEQ ID NO: 625, SEQ ID NO: 568, SEQ ID NO: 454, SEQ ID NO: 800, SEQ ID NO: 499, SEQ ID NO: 779, and SEQ ID NO: 385.

75. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least two membrane spanning regions selected from the group consisting of SEQ ID NO: 1573, SEQ ID NO: 1705, SEQ ID NO: 1707, SEQ ID NO: 1723, SEQ ID NO: 1726, SEQ ID NO: 1760, SEQ ID NO: 1764, SEQ ID NO: 1798, SEQ ID NO: 1803, SEQ ID NO: 1807, SEQ ID NO: 1889, SEQ ID NO: 1892, SEQ ID NO: 1460, SEQ ID NO: 1477, SEQ ID NO: 1499, SEQ ID NO: 1514, SEQ ID NO: 1641, SEQ ID NO: 648, SEQ ID NO: 643, SEQ ID NO: 537, SEQ ID NO: 511, SEQ ID NO: 616, SEQ ID NO: 829, SEQ ID NO: 546, SEQ ID NO: 780, SEQ ID NO: 553, SEQ ID NO: 549, SEQ ID NO: 410, SEQ ID NO: 608, SEQ ID NO: 513, SEQ ID NO: 656, SEQ ID NO: 845, SEQ ID NO: 563, SEQ ID NO: 570, SEQ ID NO: 805, and SEQ ID NO: 851.

76. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least three membrane spanning regions selected from the group consisting of SEQ ID NO: 1534, SEQ ID NO: 1564, SEQ ID NO: 1673, SEQ ID NO: 1746, SEQ ID NO: 1794, SEQ ID NO: 1843, SEQ ID NO: 1894, SEQ ID NO: 423, SEQ ID NO: 810, SEQ ID NO: 604, SEQ ID NO: 636, SEQ ID NO: 757, SEQ ID NO: 412, and SEQ ID NO: 816.

77. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least four membrane spanning regions selected from the group consisting

of SEQ ID NO: 1536, SEQ ID NO: 1544, SEQ ID NO: 1568, SEQ ID NO: 1572, SEQ ID NO: 1582, SEQ ID NO: 1738, SEQ ID NO: 1891, SEQ ID NO: 1660, SEQ ID NO: 771, SEQ ID NO: 418, SEQ ID NO: 662, SEQ ID NO: 512, SEQ ID NO: 679, SEQ ID NO: 605, SEQ ID NO: 421, SEQ ID NO: 552, SEQ ID NO: 576, and SEQ ID NO: 571.

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78. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least five membrane spanning regions selected from the group consisting of SEQ ID NO: 1793, SEQ ID NO: 1832, SEQ ID NO: 1841, SEQ ID NO: 1860, SEQ ID NO: 1486, SEQ ID NO: 725, SEQ ID NO: 565, SEQ ID NO: 717, SEQ ID NO: 536, SEQ ID NO: 647, SEQ ID NO: 409.

79. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least six membrane spanning regions selected from the group consisting of SEQ ID NO: 1465, SEQ ID NO: 1539, SEQ ID NO: 1693, SEQ ID NO: 1629, SEQ ID NO: 501, SEQ ID NO: 838, SEQ ID NO: 428, SEQ ID NO: 494, SEQ ID NO: 479, SEQ ID NO: 711, and SEQ ID NO: 722.

80. The purified polypeptide of claim 73, wherein said *H. pylori* surface or membrane polypeptide or a fragment thereof is an *H. pylori* polypeptide or a fragment thereof having at least seven membrane spanning regions selected from the group consisting of SEQ ID NO: 1540, SEQ ID NO: 1791, SEQ ID NO: 1525, SEQ ID NO: 1558, SEQ ID NO: 1655, SEQ ID NO: 1517, SEQ ID NO: 645, SEQ ID NO: 670, SEQ ID NO: 746, SEQ ID NO: 493, SEQ ID NO: 540, SEQ ID NO: 612, SEQ ID NO: 629, SEQ ID NO: 484, SEQ ID NO: 485, SEQ ID NO: 486, and SEQ ID NO: 433.

81. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 56.

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82. A vaccine composition of claim 81, further comprising a pharmaceutically acceptable carrier.

83. A vaccine composition of claim 82, wherein the pharmaceutically acceptable carrier is an adjuvant.

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84. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 81, such that treatment of *H. pylori* infection occurs.

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85. A method of claim 84, wherein the treatment is a prophylactic treatment.
86. A method of claim 84, wherein the treatment is a therapeutic treatment.
- 5 87. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 61.
- 10 88. A vaccine composition of claim 87, further comprising a pharmaceutically acceptable carrier.
89. A vaccine composition of claim 88, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 15 90. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 87, such that treatment of *H. pylori* infection occurs.
- 20 91. A method of claim 90, wherein the treatment is a prophylactic treatment.
92. A method of claim 90, wherein the treatment is a therapeutic treatment.
- 25 93. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 72.
94. A vaccine composition of claim 93, further comprising a pharmaceutically acceptable carrier.
- 30 95. A vaccine composition of claim 94, wherein the pharmaceutically acceptable carrier is an adjuvant.
- 35 96. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 93, such that treatment of *H. pylori* infection occurs.
97. A method of claim 96, wherein the treatment is a prophylactic treatment.

98. A method of claim 96, wherein the treatment is a therapeutic treatment.

99. A vaccine composition for prevention or treatment of an *H. pylori* infection comprising an effective amount of an *H. pylori* polypeptide of claim 73.

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100. A vaccine composition of claim 99, further comprising a pharmaceutically acceptable carrier.

101. A vaccine composition of claim 100, wherein the pharmaceutically acceptable carrier is an adjuvant.

102. A method of treating a subject for *H. pylori* infection comprising administering to a subject a vaccine composition of claim 99, such that treatment of *H. pylori* infection occurs.

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103. A method of claim 102, wherein the treatment is a prophylactic treatment.

104. A method of claim 102, wherein the treatment is a therapeutic treatment.

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105. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

(a) contacting a sample with a nucleic acid of claim 1 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

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(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

106. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

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(a) contacting a sample with a nucleic acid of claim 9 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and

(b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

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107. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

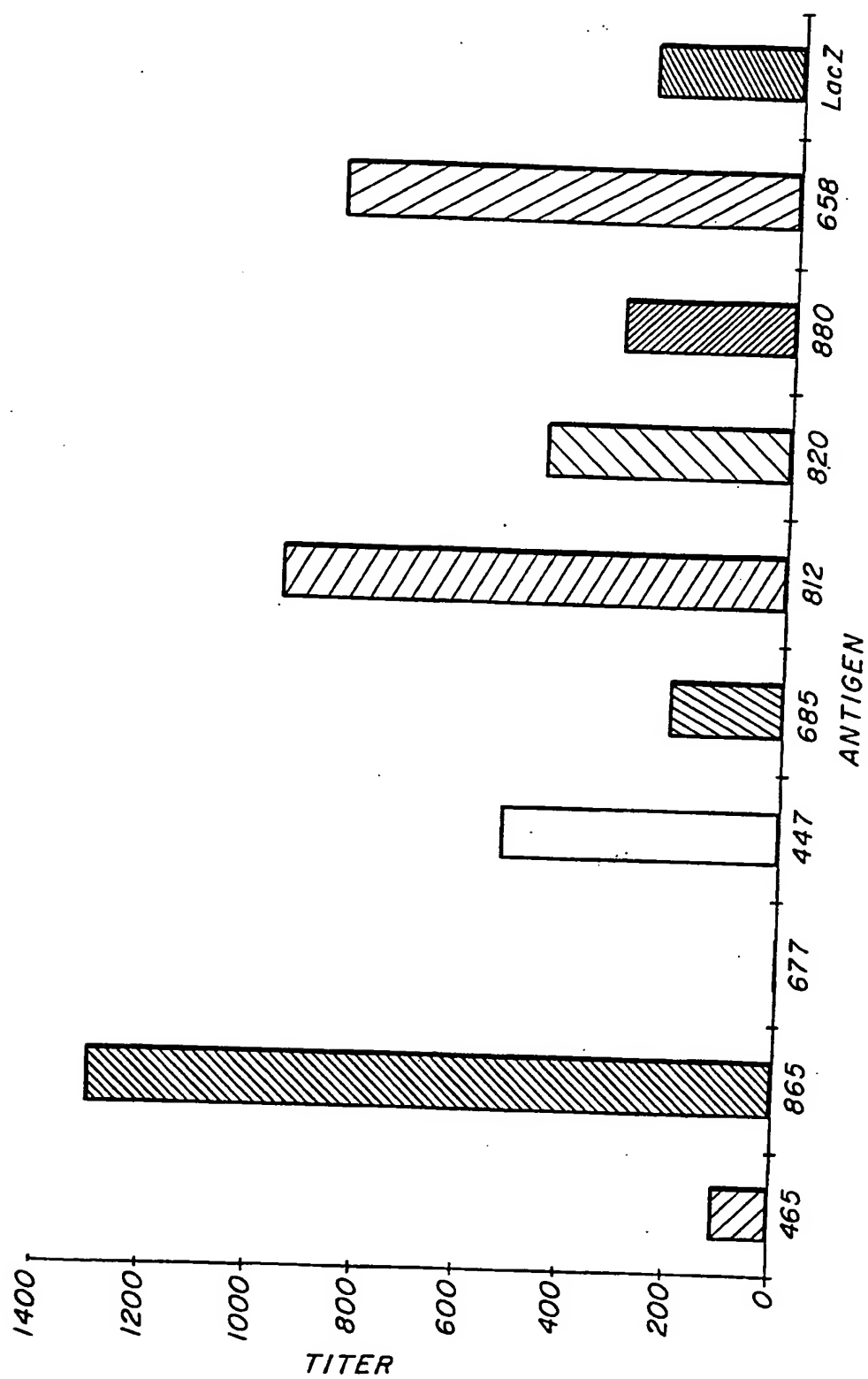
1472

- (a) contacting a sample with a nucleic acid of claim 23 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

108. A method for detecting the presence of a *Helicobacter* nucleic acid in a sample comprising:

- (a) contacting a sample with a nucleic acid of claim 27 under conditions in which a hybrid can form between the probe and a *Helicobacter* nucleic acid in the sample; and
- (b) detecting the hybrid formed in step (a), wherein detection of a hybrid indicates the presence of a *Helicobacter* nucleic acid in the sample.

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**FIG. 1**

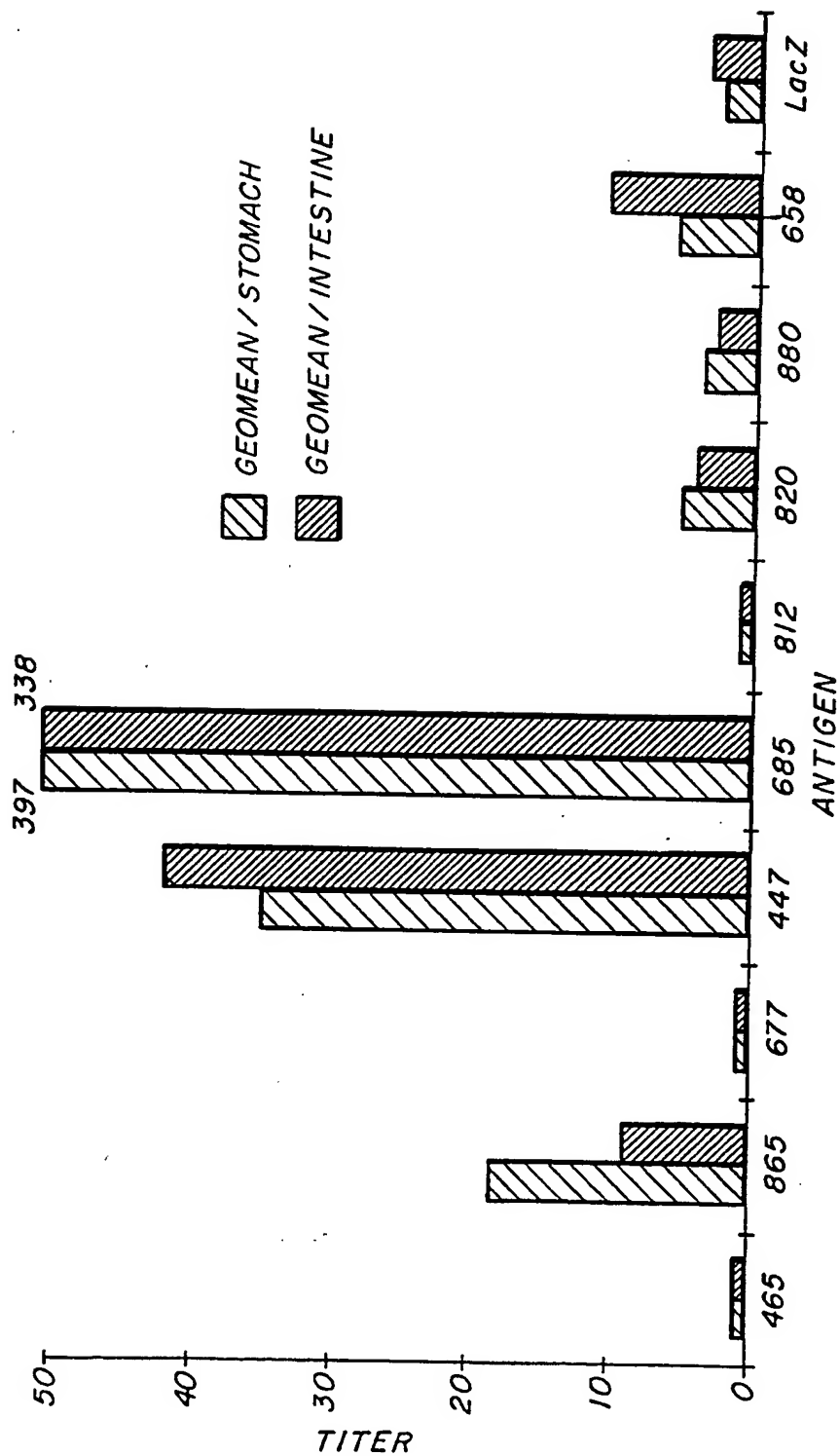


FIG. 2

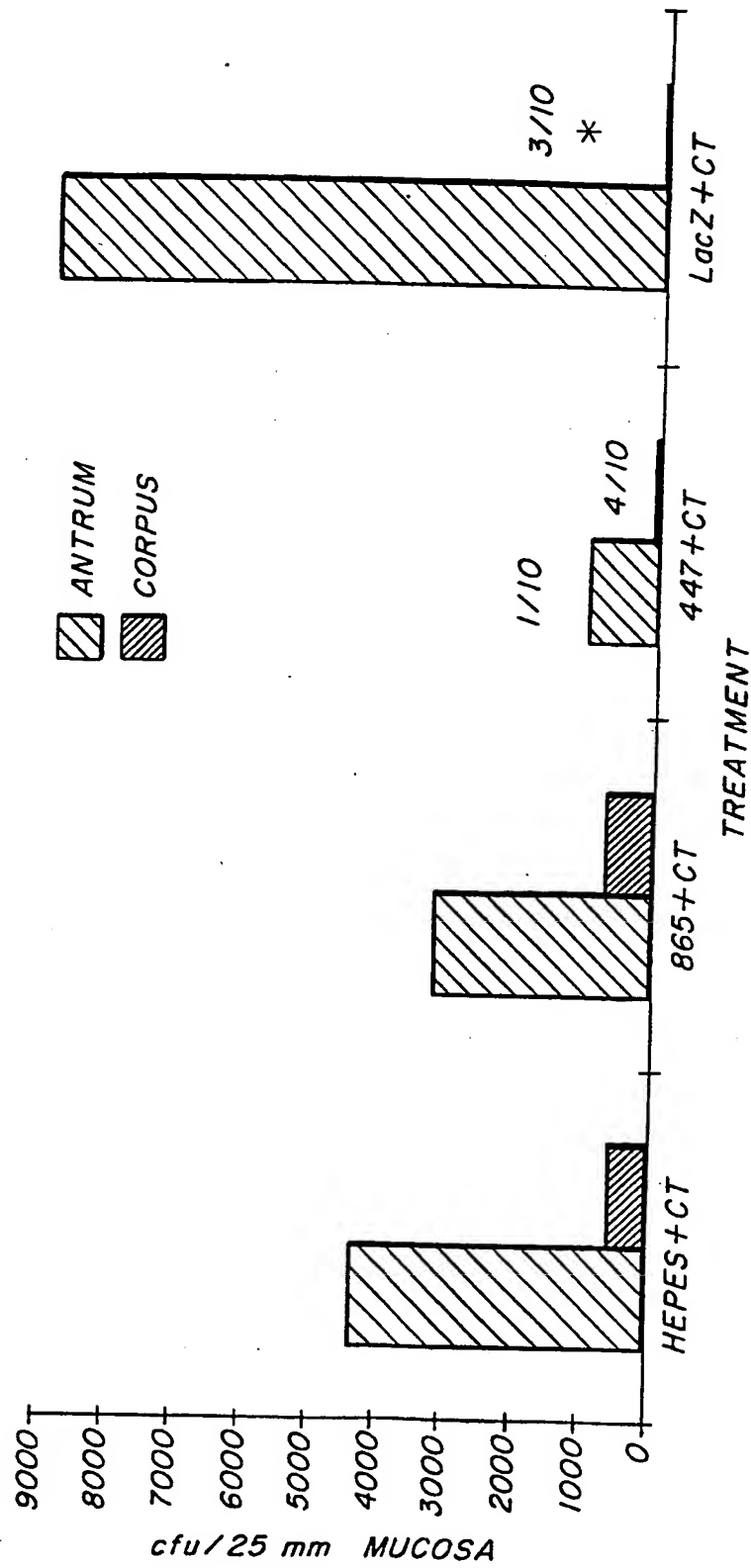


FIG. 3

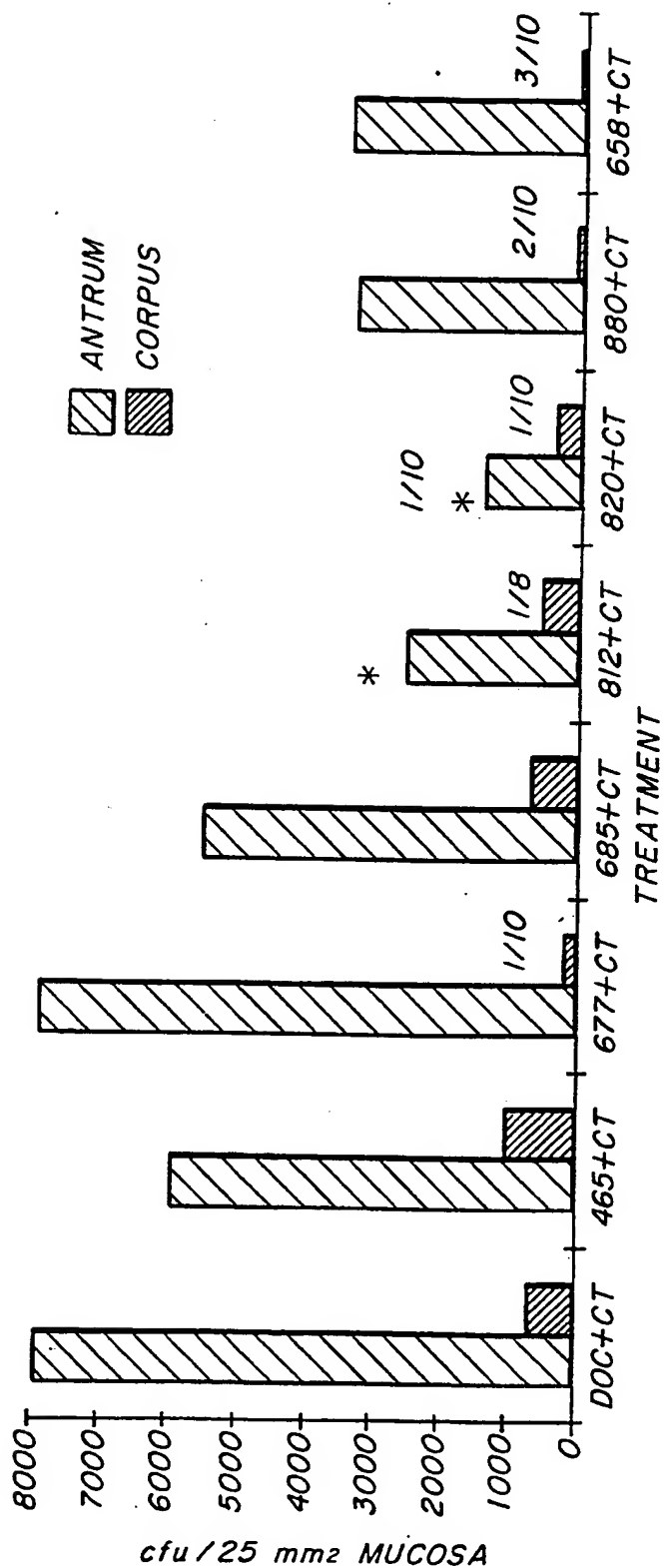


FIG. 4

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/09122

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : C12N 15/00

US CL : 514/44

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 514/44; 435/172.3; 935/6, 9, 11

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
Helicobacter pylori reading file of authorized officer.Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EMBL/GENEBANK, DIALOG, MEDLINE
search terms: Helicobacter pylori, gene?

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BUKANOV et al. Ordered cosmid library and high-resolution physical-genetic map of Helicobacter pylori strain NCTC11638. Molecular Microbiology. February 1994, Vol. 11, No. 3, pages 509-523, especially experimental procedures section pages 519-521.	1, 5, 56, 60
Y	TAYLOR et al. Construction of a Helicobacter pylori genome map and demonstration of diversity at the genome level. Journal of Bacteriology. November 1992, Vol. 174, No. 21, pages 6800-6806, especially pages 6800-6801.	1, 5, 56, 60

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* "A"	Special categories of cited documents: document defining the general state of the art which is not considered to be of particular relevance	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E"	earlier document published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search

11 SEPTEMBER 1996

Date of mailing of the international search report

23.09.1996

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/09122

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1, 5, 56 and 60

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/09122

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING

This International Search Authority has found 263 inventions claimed in the International Application covered by the claims indicated below:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack Unity of Invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be examined the appropriate additional examination fees must be paid.

The species are as follows:

Group I contains a separate DNA species for each sequence mentioned. Therefore, there is a minimum of 527 species.

Group II contains at least one polypeptide for each DNA sequence mentioned. Therefore is a minimum of 527 species in this Group.

For the species in each Group that applicant elects, a total of 10(ten) specified sequences will be searched and no more than 4(FOUR) specified sequences will be searched for each additional fee paid.

The species listed above do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2 the species lack the same or corresponding special technical features for the following reasons: There is no relationship between or among the various nucleotide and amino acid sequences mentioned in the claims.

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